



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 94446

TO: Christine Saoud

Location:

Art Unit: 1647

May 30, 2003

10B19

Case Serial Number: 901938

From: P. Sheppard

Location: CM1-1E03

Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

STIC-Biotech/Ch mLib

94446

From: Saoud, Christine
Sent: Tuesday, May 20, 2003 10:35 AM
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Subject: sequence search

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MAY 20 2003

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(STIC)

09/901,938

Please search SEQ ID NO:1 and 2 in the patent and commercial databases (no interference, please).

Thank you,

Christine Saoud
A.U. 1647
CM1 - 10E03
305-7519
mailbox in 10B19

Point of Contact
P. Sheppard

Telephone number: (703) 308-4499

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 5/30/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.4_p5_4578E
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 21:20:14 ; Search time 404 Seconds
(without alignments)
8985.696 Million cell updates/sec

Title: US-09-901-938-1

Sequence: 1 **cggcacaaaggaggaatcc**.....**tgagcacctctgtctgcct** 1612

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1612	100.0	1612	24	ABK48318	CDNA encoding human
2	1598	99.1	2770	24	AB150577	Human OST311 poly(r)
3	1256	77.9	2749	21	AAH61157	Human fibroblast g
4	1238.4	76.8	1240	22	AAH61481	Human secreted p
5	1211	75.1	1211	22	AAH28133	Nucleotide sequenc
6	1211	75.1	1211	24	ABA97195	Human 2FGF12 encod
7	1151	71.4	12300	24	AB150582	Human OST311 genom
8	912	56.6	1873	21	AAH61159	Human fibroblast g
9	798	43.5	996	22	AAH21376	Human CDNA sequenc

10	798	49.5	996	22	AAAF44266	Human PRO9628 nucleotide sequence
11	756	46.9	756	22	AAAD16366	Human sbgFCF-19b cDNA
12	756	46.9	756	22	AAH75021	Nucleotide sequence
13	756	46.9	756	22	AAH75023	Nucleotide sequence
14	756	46.9	756	24	ABN81575	Human FGF23 protein
15	756	46.9	756	24	ABL91738	Human polynucleotide
16	753	46.7	753	22	AAH76317	Human fibroblast c
17	685.6	42.5	747	24	ABL50653	Hls-OST311 DNA seqc
18	684	42.4	684	24	ABL50578	Human OST311 poly
19	674.4	41.8	690	24	ABL50654	MK-OST311 DNA seq
20	659.2	40.9	805	21	AAAC61158	Monkey fibroblast
21	537	33.3	537	21	AAAC61155	Human fibroblast 9
22	534	33.1	534	21	AAAC61160	Human fibroblast 9
23	528	32.8	753	22	AAH28134	Degenerate sequence
24	528	32.6	753	24	ABA97196	Human ZFGF12 degen
25	493.2	30.6	531	21	AAAC61156	Monkey fibroblast
26	465	28.8	465	24	ABL50579	Human OST311 poly
27	457.4	28.4	1559	24	ABK45312	cDNA encoding mouse
28	428	26.6	756	22	AAH75032	Nucleotide sequence
29	428	26.6	756	22	ABL50581	Nucleotide sequence
30	293.4	18.2	543	24	ABL50581	Mouse OST311 poly
31	219	13.6	219	24	ABL50580	Human OST311 poly
32	74	4.6	630	22	AAAF89921	Nucleotide sequence
33	73.2	4.5	624	22	AAD09152	Human fibroblast 9
34	72.8	4.5	514	22	AAAF76715	Human fibroblast 9
35	72.6	4.5	651	24	ABL91719	Human polynucleotide
36	72.6	4.5	2133	20	AAXS2224	Protein PRO53 cDN
37	72.6	4.5	2133	20	AAAX2430	FGF homologue PRO
38	72.6	4.5	2137	20	AAV74455	Human PRO53 cDNA
39	72.6	4.5	2137	21	AAAC58599	Human PRO533 prote
40	72.6	4.5	2137	21	AAA30028	Human PRO533 nucle
41	72.6	4.5	2137	22	AAAF58498	PRO533 coding sequ
42	72.6	4.5	2137	22	AAAC87022	Nucleotide sequence
43	72.6	4.5	2137	22	AAAF73389	Human PRO533 cDN
44	72.6	4.5	2137	24	ABL95592	Human angiotensin
45	72.6	4.5	2137	24	ABL86110	Human PRO533 cDNA

ALIGNMENTS

RESULT 1
ABK48318

ID	ABK48318	standard; CDNA; ;
XX		
AC	ABK48318;	
XX		
DT	02-JUL-2002	(first entry)

DE cDNA encoding human fibroblast growth factor-23 (FGF23).

KM fibroblast growth factor 23; FGF23; hypophosphataemic disorder;
KM autosomal dominant hypophosphataemic rickets; ADHR; fibrous dysplasia;
KM X-linked hypophosphataemic rickets; XLHR; tumour induced osteomalacia;
TIO; hereditary hypophosphataemic rickets with hypercalcaemia; HHRH;
KM hypophosphataemic bone disease; HBD; epidermal nevus syndrome;
KM nephrocalcinosis; hyperphosphataemic disorder; mild renal insufficiency;
KM tumour calcinosis; osteopetrosis; dermatomyositis; human; gene; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
ET	CDS	147 903

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    / *tag= a
    /product= "EGF23"

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FT	/note="Fibroblast growth factor 23"
FT	
FT	sig_peptide
	147..218

PN WO200208271-A1

XX 31-JAN-2002.
 PD 10-JUL-2001; 2001WO-US21738.
 XX 19-JUL-2000; 2000US-219137P.
 PR (ADRE-) ADVANCED RES & TECHNOLOGY INST.
 XX (UWMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
 PA Ecoms M, White K, Strom TM, Weitingger T;
 PI MPI: 2002-329399/35.
 XX P-PSDB; AAU79355.
 DR Novel fibroblast growth factor 23, and polymucineid encoding the
 PT mild renal insufficiency or tumoural calcinosis, or coronary artery
 PT disease
 XX Claim 2; Fig 5A; 130bp; English.
 PS
 CC The invention describes an isolated polypeptide (I) comprising a
 CC fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant,
 CC homologue or fragment. (I) is useful for treatment of a hypophosphataemic
 CC disorder such as autosomal dominant hypophosphataemic rickets (ADHR),
 CC X-linked hypophosphataemic rickets (XLH), hereditary hypophosphataemic
 CC rickets with hypercalciuria (HHRH), hypophosphataemic bone disease (HBD),
 CC epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia
 CC (TIO), and nephrolithiasis. (I) can also be used in treatment of a
 CC hypophosphataemic disorder such as mild renal insufficiency and tumoural
 CC calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving
 CC deposition of calcium and phosphate in the arteries or soft tissues of
 CC mammal, coronary artery disease may also be treated using methods
 CC described in the invention. Preferably, the nucleic acid or the
 CC polypeptide comprises a mutation that confers increased stability on
 CC FGF23 polypeptide. The polymucineid encoding (I) can be used in gene
 CC therapy to treat diseased individuals. This sequence encodes the novel
 CC human fibroblast growth factor 23 (FGF23) studied in the invention.
 XX
 SQ Sequence 1612 BP; 405 A; 462 C; 418 G; 327 T; 0 other;
 Query Match 100.0%; Score 1612; DB 24; Length 1612;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 GATACCTCTGATGATGATTTTCAAGGCAATTTTGGATCACTATTTCAGCCCGAGA 480
 Db 421 GATACCTCTGATGATGATTTTCAAGGCAATTTTGGATCACTATTTCAGCCCGAGA 480
 QY 481 ACTGAGGTTTCAACCAAGACGCTGGAAAAAGGGTACAGCTTACACTCTCTCAGT 540
 Db 481 ACTGAGGTTTCAACCAAGACGCTGGAAAAAGGGTACAGCTTACACTCTCTCAGT 540
 QY 541 ATGACCTCTGATGATGATTTTCAAGGCAATTTTGGATCACTATTTCAGCCCGAGA 600
 Db 541 ATGACCTCTGATGATGATTTTCAAGGCAATTTTGGATCACTATTTCAGCCCGAGA 600
 QY 601 CCGGTAATCCAGTTCTCTTCCGAGAGAGATCCCTTATTCATTCACTTCAACACC 660
 Db 601 CCGGTAATCCAGTTCTCTTCCGAGAGAGATCCCTTATTCATTCACTTCAACACC 660
 QY 661 CCATACCAAGCGCGACACCCGAGAGCGCGAGAGACGCTCGAGAGCGGACCCCTGAACG 720
 Db 661 CCATACCAAGCGCGACACCCGAGAGCGCGAGAGACGCTCGAGAGCGGACCCCTGAACG 720
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 Db 721 TGCTGAAGCCCGGCGCGGATGACCCCGGCGCGGCTCTCTTCAAGAGCTCTCCGA 780
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 QY 901 AGGGTGGTGGAGGGGACCTCTTTAACCATTCCCTCAGCAACGACGCTTTCCCAAG 960
 Db 901 AGGGTGGTGGAGGGGACCTCTTTAACCATTCCCTCAGCAACGACGCTTTCCCAAG 960
 QY 961 GACCAAGTCCCTTGAAGTCCGAGAGTGGGAAAGGAGAGAGGAGGAGGAGGAGGAGG 1020
 Db 961 GACCAAGTCCCTTGAAGTCCGAGAGTGGGAAAGGAGAGGAGGAGGAGGAGGAGGAGG 1020
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 Db 1021 TGCTTCTGAGGGTCCCTTCAAGAGAGTCTGTGAGAACCACTTTGAGGCGCAAGT 1080
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 QY 1441 ACACTACTTTCAAGCTTCTCTCTTCAAGCATCTGAGGAGGAGGAGGAGGAGGAGGAG 1500
 Db 1441 ACACTACTTTCAAGCTTCTCTCTTCAAGCATCTGAGGAGGAGGAGGAGGAGGAGGAG 1500


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Db 541 GCGCGGCGGAGAGAGCTTCTCTGCGAGGAGTAAAGCCAGCCCTCTCTCCAGTTCTG 600
Qy 621 TCCGAGAGAGAGAGAGTCCCTTAATTCATTCAACACCCCATACAGCGGCGGACACC 680
Db 601 TCCGAGAGAGAGAGAGTCCCTTAATTCATTCAACACCCCATACAGCGGCGGACACC 660
Qy 681 CGAGAGCGCGGAGAGAGTCCGAGCGGAGACCCCTGAACTGCTGAAGCCCGGCGG 740
Db 661 CGAGAGCGCGGAGAGAGTCCGAGCGGAGACCCCTGAACTGCTGAAGCCCGGCGG 720
Qy 741 ATGAGCGCGCGGCGGCTCTCTGTTCAAGAGGCTCCCGAGCGCGGAGAGAGAGCCCG 800
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Qy 801 ATGAGCGCGGAGAGAGTCCGAGCGGAGAGTCCGAGAGAGAGAGAGAGAGAGAGAG 860
Db 781 ATGAGCGAGAGAGAGAGTCCGAGCGGAGAGTCCGAGAGAGAGAGAGAGAGAGAGAG 840
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Db 841 AGGAGCGCGGAGAGAGTCCGCGGCGGCGGAGAGTCCGAGAGAGAGAGAGAGAGAG 900
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Db 1021 CACAGAGAGTCTCTGTAGAGAGAGAGTCCGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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Db 1201 CCTCTTATATCACTTTTAAAGCATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1240

RESULT 5
AAH28133
ID AAH28133 standard; DNA; 1211 BP.
XX
XX
XX AAH28133;
AC
XX
XX 05-SEP-2001 (first entry)
DT
XX
XX Nucleotide sequence of fibroblast growth factor homologue zFGF12.
DE
XX
XX Fibroblast growth factor; FGF; zFGF12; chromosome 12; 12q.1.3;
KM neuronal cell; prostatic cell; pancreatic cell; haematopoietic cell;
KW hyperplasia; regeneration; diabetes; amyotrophic lateral sclerosis;
KM stroke; angiogenesis; wound healing; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH CDS 115..870
FT /tag= a
FT /product= "fibroblast growth factor homologue zFGF12"
FT sig_peptide 115..186
FT /tag= b
FT mat_peptide 187..870
FT /tag= c

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XX WO200149740-A1.
PN
XX
XX 12-JUL-2001.
PD
XX
XX 04-JAN-2001; 2001MO-US00238.
PF
XX
XX 05-JAN-2000; 2000US-0478062.
PR
XX
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Conklin DC;
PI
XX
XX WPI; 2001-418357/44.
DR
XX
XX P-PSDB; AAB84652.
DQ
XX
XX A fibroblast growth factor homologue polypeptide zFGF12 and the nucleic
PT acids that encode it, useful for preventing, diagnosing and controlling
PT e.g. diabetes, amyotrophic lateral sclerosis, strokes, angiogenesis
PT and wound healing -
PS
XX
XX Claim 16; Page 58-60; 66pp; English.
XX
XX The present sequence encodes a human fibroblast growth factor (FGF)
CC homologue, designated zFGF12. The zFGF12 polypeptides contain a motif
CC (see AAB84654) that occurs in all known members of the FGF family, which
CC is unique to these proteins. This motif is highly conserved in all
CC members of the FGF family, however, zFGF12 appears to be unique in that
CC the conserved Glu is a His (residue 117) substituting a basic amino
CC acid (aa) residue for an acidic aa residue. The zFGF12 gene is mapped
CC to chromosome 12, location 12q.1.3. zFGF12 may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate FGF expression. Disorders and processes that may be
CC prevented, diagnosed, and treated include, for example proliferation
CC of neuronal, prostatic and pancreatic tissue cells, growth and
CC differentiation of haematopoietic cells, hyperplasia and regeneration,
CC diabetes, amyotrophic lateral sclerosis, strokes, angiogenesis and
CC wound healing.
XX
XX
XX Sequence 1211 BP; 273 A; 380 C; 321 G; 237 T; 0 other;
SQ
Query Match 75.1%; Score 1211; DB 22; Length 1211;
Best Local Similarity 100.0%; Pred. No. 2.8e-282;
Matches 1211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 93 CCGAGAGAGTCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 152
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Qy 153 GGGGCGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCT 212
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Qy 213 AGAGCTATCCCAATGCTCCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 272
Db 181 AGAGCTATCCCAATGCTCCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 240
Qy 273 TCACAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 332
Db 241 TCACAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 333 GGGGAGCCCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
Db 301 GGGGAGCCCATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 393 GTGGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 452
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DB 421 TTGGATCACTATTTCAGACCCGGAGAACTGAGGTTCCAACACAGACCGCTGGAAAC 480
QY 513 GGGTACAGCGTCACTCACTCTCTCATGATCATCTTCTGATGAGTGGGCGGGCGAAG 572
DB 481 GGGTACAGCGTCACTCACTCTCTCATGATCATCTTCTGATGAGTGGGCGGGCGAAG 540
QY 573 AGAGCTTCTGCGGAGGATGAACCCACCCCGTACTCCAGTTCTGTCTCCGAGAGAC 632
DB 541 AGAGCTTCTGCGGAGGATGAACCCACCCCGTACTCCAGTTCTGTCTCCGAGAGAC 600
QY 633 GAGATCCCTTAATTCATTCAACACCCCATACACGCGGGGACACCCGAGAGCGCGAG 692
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QY 753 CCGGCTCTGTTTCAAGAGGCTCCGAGCGCGAGGACAAACAGCCGATGCGCATGAC 812
DB 721 CCGGCTCTGTTTCAAGAGGCTCCGAGCGCGAGGACAAACAGCCGATGCGCATGAC 780
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QY 873 GGTGCGCGCCCTTGGCGAAGTTCACTAGGGGTGCTGAAAGGGGACCCCTTTAACCA 932
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DB 901 TCCCTGAGCAAGCGAGCTCTTCCCAAGAGACAGAGCTCTTGAAGTTCCAGAGTGGAA 960
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DB 1141 GTAGAGAGAGGGGTCTCTCCCAATATTTCTCTCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1233 TTTTAAGCAT 1243
DB 1201 TTTTAAGCAT 1211

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RESULT 6
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ID ABA97195 standard; DNA; 1211 BP.

AC ABA97195;
XX 18-JUN-2002 (first entry)
XX Human zFGF12 encoding sequence.
DE zFGF12; human; fibroblast growth factor; FGF; vulnery; chemotherapy;
KW lung injury; epithelial cell; mesenchymal cell; ds.
XX Homo sapiens.
OS Key
XX Location/Qualifiers

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FT CDS 115..870
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PN US2001044525-A1.
PD 22-NOV-2001.
PF 04-JAN-2001; 2001US-0754634.
PR 05-JUN-2000; 2000US-174582P.
PA (CONK/) CONKLIN D C.
XX Conklin DC;
XX WPI: 2002-105575/14.
XX P-PSDB; ABB08352.
XX DR
XX New fibroblast growth factor, designated zFGF12 is for promoting wound
XX healing, protecting and stimulating epithelial cells after chemotherapy
XX PT or radiation, and stimulating lung epithelial cells after premature
XX birth or injury
XX PS Claim 16; Page 21-22; 34pp; English.
XX CC
XX The invention relates to a fibroblast growth factor polypeptide,
XX designated zFGF12, comprising a sequence at least 95% identical to
XX residues 25 to 251 of the 251 amino acid sequence, given in the
XX CC specification. The activity of the fibroblast growth factor of the
XX CC invention may be described as vulnery. zFGF12 can be used to promote
XX CC wound healing of the epidermis, to protect and promote recovery of
XX CC epithelial cells in the gastrointestinal tract, small intestine and oral
XX CC mucosa after chemotherapy or radiation, and to stimulate lung epithelial
XX CC cells after lung injury or complications in neonates following premature
XX CC birth. The polypeptide can also be used to modulate proliferation and
XX CC function of epithelial cells of prostate, cornea, mammary and kidney
XX CC tissue. The polypeptide is also useful to stimulate proliferation of
XX CC cultured mesenchymal cells and to identify new family members. The
XX CC current sequence represents the human zFGF12 encoding sequence.
SQ Sequence 1211 BP; 273 A; 380 C; 321 G; 237 T; 0 other;

```

Query Match 75.1%; Score 1211; DB 24; Length 1211;
Best Local Similarity 100.0%; Pred. No. 2.8e-282;
Matches 1211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 TCACACAGCTACTTGAAGAGAGAGAAAGCCAGTAAAGGCTGGGCGAGAGAGTC 92
DB 1 TCACACAGCTACTTGAAGAGAGAGAAAGCCAGTAAAGGCTGGGCGAGAGAGTC 60
QY 93 CCGACAGAGAGTGTCAAGTTTCAATTCAGACACAGCCACTCAGAGCAGGCGACAGATGTTG 152
DB 61 CCGACAGAGAGTGTCAAGTTTCAATTCAGACACAGCCACTCAGAGCAGGCGACAGATGTTG 120
QY 153 GGGGCGCGCTCAGGCTGTGGGTGTGTGCTTGTGACAGGCTGTGACAGATGAGCGTCTC 212
DB 121 GGGGCGCGCTCAGGCTGTGGGTGTGTGCTTGTGACAGGCTGTGACAGATGAGCGTCTC 180
QY 213 AGAGCTATCCCAATGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 272
DB 181 AGAGCTATCCCAATGCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 273 TACACAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 332
DB 241 TACACAGCAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

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Db 199 AATCTAGACACGACCACTAGAGCAGGCGACGATGTTGGGGGCCCCGCTCAGGCTCTGG 258
Qy 174 GTCTGTGCTTTGTGCAAGGCTGTGAGCATGAGCGTCTCAGAGCCTATCCCATGCTCC 233
Db 259 GTCTGTGCTTTGTGCAAGGCTGTGAGCATGAGCGTCTCAGAGCCTATCCCATGCTCC 318
Qy 234 CCACTGTGCTTTGTGCAAGGCTGTGAGCATGAGCGTCTCAGAGCCTATCCCATGCTCC 293
Db 319 CCACTGTGCTTTGTGCAAGGCTGTGAGCATGAGCGTCTCAGAGCCTATCCCATGCTCC 378
Qy 294 AGCTACACCTGAGATCAGACCAAGATGAGCGATGAGCGGAGCCCATCAGACCATC 353
Db 379 AGCTACACCTGAGATCAGACCAAGATGAGCGATGAGCGGAGCCCATCAGACCATC 438
Qy 354 TACAGTCCCTGATGATCAGATCAGAGGATGAGCGTCTTGTGATTAAGGTGTATG 413
Db 439 TACAGTCCCTGATGATCAGATCAGAGGATGAGCGTCTTGTGATTAAGGTGTATG 498
Qy 414 AGCAGAAAGATCCTCTGATGATGATTTTCAAGGCAACATTTTGAATCAGATTTTGCAC 473
Db 499 AGCAGAAAGATCCTCTGATGATGATTTTCAAGGCAACATTTTGAATCAGATTTTGCAC 558
Qy 474 CCGGAGAACTGAGGTTCCAAACAGACGCTGGAAGAAAGGATCCCTTAATTCACCTCT 533
Db 559 CCGGAGAACTGAGGTTCCAAACAGACGCTGGAAGAAAGGATCCCTTAATTCACCTCT 618
Qy 534 CCTCAGTATCATTCTCTGATGATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 593
Db 619 CCTCAGTATCATTCTCTGATGATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 678
Qy 594 AACCCACCCCGTATCTCCAGTCTCTGTCCGAGGAAAGAGATCCCTTAATTCACCTCT 653
Db 679 AACCCACCCCGTATCTCCAGTCTCTGTCCGAGGAAAGAGATCCCTTAATTCACCTCT 738
Qy 654 AACAACCCCACTACAGGCGGAGCAACCCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 713
Db 739 AACAACCCCACTACAGGCGGAGCAACCCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 798
Qy 714 CTGAACGCTGCTGAAGCCCGGAGCGGAGTGAACCCGAGGCGGAGGAGGAGGAGGAGGAGG 773
Db 799 CTGAACGCTGCTGAAGCCCGGAGCGGAGTGAACCCGAGGCGGAGGAGGAGGAGGAGGAGG 858
Qy 774 CTCGCCAGCGCCGAGGAGCAACAGCCGATGAGCAGTGAACCATTAAGGAGGAGGAGGAGG 833
Db 859 CTCGCCAGCGCCGAGGAGCAACAGCCGATGAGCAGTGAACCATTAAGGAGGAGGAGGAGG 918
Qy 834 GGTGAGGTGAACGACGACGCTGAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 893
Db 919 GGTGAGGTGAACGACGACGCTGAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 978
Qy 894 TTTCATCTAGGAGGAGGAGG 911
Db 979 TTTCATCTAGGAGGAGGAGG 996

RESULT 10
AAAF4266
ID AAF4266 standard; cDNA; 996 BP.
AC AAF4266;
XX
XX 02-APR-2001 (first entry)
DE Human PRO9828 nucleotide sequence SEQ ID NO:510.
XX
XX Human; secreted and transmembrane protein; PRO; cytosolic;
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay; ss.
OS Homo sapiens.
XX
XX WO200073454-A1.
XX

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```

PD 07-DEC-2000.
XX
XX 30-MAR-2000; 2000MO-US08439.
PF
XX
PR 02-JUN-1999; 99MO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99MO-US21090.
PR 15-SEP-1999; 99MO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99MO-US28313.
PR 01-DEC-1999; 99MO-US28301.
PR 16-DEC-1999; 99MO-US30095.
PR 20-DEC-1999; 99MO-US30911.
PR 05-JAN-2000; 2000MO-US00219.
PR 06-JAN-2000; 2000MO-US00376.
PR 11-FEB-2000; 2000MO-US03565.
PR 18-FEB-2000; 2000MO-US04341.
PR 22-FEB-2000; 2000MO-US04414.
PR 24-FEB-2000; 2000MO-US04914.
PR 24-FEB-2000; 2000MO-US05004.
PR 02-MAR-2000; 2000MO-US05841.
PR 15-MAR-2000; 2000MO-US06884.
PR 20-MAR-2000; 2000MO-US07377.

(GETH ) GENENTECH INC.
XX
XX Aabkenazi AJ, Baker KP, Botstein D, Deansoyers L, Eaton DL;
XX Ferrara N, Fong S, Gether H, Gerlitsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurley AL, Kijavrin IU, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI: 2001-032160/04.
DR P-PSDB; AAB65297.
XX
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX PT bioactive molecules such as toxins, radiolabels or antibodies, to
XX PT specific cells, to cause targeted cell death -
XX
XX
XX Claim 2; Fig 323; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
XX CC can be used for targeted delivery of bioactive molecules, such as
XX CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX CC sequences, and their fragments, can be used as hybridisation probes, in
XX CC chromosomal and gene mapping, and in the generation of anti-sense RNA
XX CC and DNA. They may also be used to produce transgenic animals which are
XX CC used to develop and screen therapeutically useful reagents. The PRO
XX CC nucleotide and protein sequence can be used for tissue typing and in
XX CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
XX CC AAF4270 to AAF4470 represent PCR primers and hybridisation probes used
XX CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
XX CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
XX CC sequences given in the exemplification of the present invention.
XX
XX Sequence 996 BP; 222 A; 320 C; 260 G; 194 T; 0 other;
XX
XX
XX Query Match 49.5%; Score 798; DB 22; Length 996;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-182;
XX Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 114 AATCTAGACACGACCACTAGAGCAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 173
XX 199 AATCTAGACACGACCACTAGAGCAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 258
Qy 174 GTCTGTGCTTTGTGCAAGGCTGTGAGCATGAGCGTCTCAGAGCCTATCCCATGCTCC 233

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QY 267 CACCTGTACACAGCCAGCAGGAGACGATACCTGCAGATCCAAAGATGGCCAT 326
DB 121 CACCTGTACACAGCCAGCAGGAGACGATACCTGCAGATCCAAAGATGGCCAT 180
QY 327 GGGGATGGGCCCCCATTCAGACCATCTACAGTGCCTGATGATCAGAGATGCT 386
DB 181 GGGGATGGGCCCCCATTCAGACCATCTACAGTGCCTGATGATCAGAGATGCT 240
QY 387 GGGTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTTCGATGATTTCAAGGC 446
DB 241 GGGTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTTCGATGATTTCAAGGC 300
QY 447 AACATTTTGGATCACAATTTTGCACCCGAGAGATGAGTTTCAACACAGAGCTG 506
DB 301 AACATTTTGGATCACAATTTTGCACCCGAGAGATGAGTTTCAACACAGAGCTG 360
QY 507 GAAAAAGGGTACAGACCTTACCACTCTCTCAAGTACCTTCTGATCACTTGGGCGG 566
DB 361 GAAAAAGGGTACAGACCTTACCACTCTCTCAAGTACCTTCTGATCACTTGGGCGG 420
QY 567 GCGAAGAGAGCTTCTCTGCGAGGAGTAAACCCACCCGTAATCTCCAGTTCTGCTCCG 626
DB 421 GCGAAGAGAGCTTCTCTGCGAGGAGTAAACCCACCCGTAATCTCCAGTTCTGCTCCG 480
QY 627 AAGAAAGAGATCCCTTAATTCACTTCAACACCCCATACAGGGGGGCAACCCGAGC 686
DB 481 AAGAAAGAGATCCCTTAATTCACTTCAACACCCCATACAGGGGGGCAACCCGAGC 540
QY 687 GCGAGAGAGACCTCGAGAGCGGAGACCCCTGAGAGCTGTAAGCCCGGCGCGGATGAC 746
DB 541 GCGAGAGAGACCTCGAGAGCGGAGACCCCTGAGAGCTGTAAGCCCGGCGCGGATGAC 600
QY 747 CCGGCCCCCGGCTCTCTGTTTCAAGAGCTCCCGAGCGCGGAGAGCAACAGCCGATGCGC 806
DB 601 CCGGCCCCCGGCTCTCTGTTTCAAGAGCTCCCGAGCGCGGAGAGCAACAGCCGATGCGC 660
QY 807 AGTGAACCCATTAGGGGTGGTCAAGGGCGGTGAGTGAACCGAGCTGGGGGAGACGGGC 866
DB 661 AGTGAACCCATTAGGGGTGGTCAAGGGCGGTGAGTGAACCGAGCTGGGGGAGACGGGC 720
QY 867 CCGAAGAGCTGCGGCGCCCTTCGCGCAAGTTCACTAG 902
DB 721 CCGAAGAGCTGCGGCGCCCTTCGCGCAAGTTCACTAG 756

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RESULT 12
AAH75021
ID AAH75021 standard; DNA; 756 BP.
XX
AC AAH75021;
XX
DT 29-OCT-2001 (first entry)
XX
XX Nucleotide sequence of human fibroblast growth factor 23 (FGF-23).
XX
KM Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer;
KM congenital defect; fertility; abnormal growth; thymus function;
KM leukemia; lymphoma; autoimmune disease; proliferative disorder;
KM differentiation disorder; central nervous system disorder; infarction;
KM Parkinson's disease; Alzheimer's disease; Crohn's disease; inflammation;
KM intestinal wound; motility disorder; absorption disorder; stroke;
KM congenital malformation; ischemic vascular disease; myocardial ischemia;
KM peripheral vascular disease; renal artery disease; bone disease;
KM musculoskeletal disease; skeletal myopathy; arthritis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..756
FT /tag= a
FT /product= "fibroblast growth factor 23 (FGF-23"
XX
FN MO20016596-A2.

```

XX
PD 13-SEP-2001.
XX
XX 07-MAR-2001; 2001WO-US07469.
XX
XX 08-MAR-2000; 2000US-0187854.
PR 18-SEP-2000; 2000US-0233368.
PR 05-DEC-2000; 2000US-0251649.
XX
XX (CHIR ) CHIRON CORP.
PA (KYOU ) UNIV KYOTO.
XX
PI Itoh N, Kavanagh MW,
XX
XX WPI; 2001-522948/57.
DR P-PSDB; AAG63944.
XX
PT Isolated nucleic acids encoding the human and murine fibroblast growth
PT factor 23, useful in the treatment of a condition characterized by
PT inadequate function of placental cells (e.g. congenital defects) and
PT the thymus (e.g. leukemia) -
XX
PS Claim 2; Fig 3; 77pp; English.
XX
CC The present sequence encodes fibroblast growth factor 23 (FGF-23).
CC Human FGF-23 polynucleotides and polypeptides are useful for treating
CC a patient suffering from traumatic injury or a condition characterized
CC by dysfunction of or injury to skin cells, a condition characterized by
CC inadequate function of placental cells (e.g. congenital defects),
CC fertility, or abnormal growth), a condition characterized by inadequate
CC function of the thymus (e.g. leukemia, lymphoma, autoimmune disease,
CC proliferative disorder of the thymus, or differentiation disorder of
CC the thymus), or a condition characterized by central nervous system
CC disorder (e.g. Parkinson's disease or Alzheimer's disease). The human
CC FGF-23 polynucleotide and polypeptide are also useful in the treatment
CC of Crohn's disease, healing of intestinal wounds, ulcers, inflammation,
CC injuries and surgical anastomoses, motility and absorption disorders,
CC and congenital malformations of the intestine. They are also useful for
CC treating ischemic vascular diseases (e.g. myocardial ischemia/infarction,
CC peripheral vascular disease, renal artery disease, stroke) and
CC musculoskeletal disease characterized by loss of function, inadequate
CC function or death of skeletal muscle cells, bone cells or supporting
CC cells (e.g. skeletal myopathies, bone disease, or arthritis).
XX
SQ Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;

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Query Match 46.9%; Score 756; DB 22; Length 756;
Best Local Similarity 100.0%; Pred. No. 1.5e-172;
Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 147 ATGTTGGGGGCGCGCTCAGGCTGGGTCTGCTGCTTGTGAGAGCTCTGCAGCATGAGC 206
DB 1 ATGTTGGGGGCGCGCTCAGGCTGGGTCTGCTGCTTGTGAGAGCTCTGCAGCATGAGC 60
QY 207 GTCTCAGAGCTATCCCATGCTCTCCCACTGCTCGGCTCGAGCTGGGGGTGGCCATG 266
DB 61 GTCTCAGAGCTATCCCATGCTCTCCCACTGCTCGGCTCGAGCTGGGGGTGGCCATG 120
QY 267 CACCTGTACACAGCCAGCAGGAGAAAGCTTCAACCTGACAGATCCCAAGATGGCCAT 326
DB 121 CACCTGTACACAGCCAGCAGGAGAAAGCTTCAACCTGACAGATCCCAAGATGGCCAT 180
QY 327 GGGGATGGGCCCCCATTCAGACCATCTACAGTGCCTGATGATCAGAGATGCT 386
DB 181 GGGGATGGGCCCCCATTCAGACCATCTACAGTGCCTGATGATCAGAGATGCT 240
QY 387 GGGTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTTCGATGATTTCAAGGC 446
DB 241 GGGTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTTCGATGATTTCAAGGC 300
QY 447 AACATTTTGGATCACAATTTTGCACCCGAGAGATGAGTTTCAACACAGAGCTG 506
DB 301 AACATTTTGGATCACAATTTTGCACCCGAGAGATGAGTTTCAACACAGAGCTG 360

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Qy	687	GC	CGAGGAGACGACTCGGAGCGGAGACCCCTTAAGTGTAAGCCCGGAGCCCGGATGACC	746
Db	541	GC	CGAGGAGACGACTCGGAGCGGAGACCCCTTAAGTGTAAGCCCGGAGCCCGGATGACC	600
Qy	747	CC	GGCCCGCGGACCTCTGTTCACAGAGACTCCGAGCGCCGAGACAACAGCCGATGGCC	806
Db	601	CC	GGCCCGCGGACCTCTGTTCACAGAGACTCCGAGCGCCGAGACAACAGCCGATGGCC	660
Qy	807	AG	TGACCCATTAGGGGTGTCAGGGGCGGTTCAGTGAACACGACCGTGGGGGAAACGGGC	866
Db	661	AG	TGACCCATTAGGGGTGTCAGGGGCGGTTCAGTGAACACGACCGTGGGGGAAACGGGC	720
Qy	867	CC	GGAAGGCTGCGCGCCCTTCGCAAGTTCATCTAG	902
Db	721	CC	GGAAGGCTGCGCGCCCTTCGCAAGTTCATCTAG	756
RESULT 14				
ID	ABN81575	ABN81575 standard, cDNA, 756 BP.		
XX	AC	ABN81575		
XX	ABN81575;			
XX	28-AUG-2002	(first entry)		
XX	DE	Human FGF23 protein encoding cDNA SEQ ID NO 1.		
XX	DE	Human, FGF23; haemostatic; hyperphosphataemia; gene therapy; gene; ss.		
XX	OS	Homo sapiens.		
XX	Key	Location/Qualifiers		
XX	FF	1..756		
XX	FT	/*tag= a		
XX	FT	/product= "FGF23 protein"		
XX	FN	WO200252009-A1.		
XX	PD	04-JUL-2002.		
XX	PP	26-DEC-2001; 2001WO-JP11482.		
XX	PR	26-DEC-2000; 2000JP-0396316.		
XX	PR	29-MAY-2001; 2001JP-0161370.		
XX	PA	(CHUS) CHUGAI SEIYAKU KK.		
XX	PI	Itoh H, Fukushima N, Saico H, Kusano K;		
XX	PI	WPI; 2002-508891/54.		
XX	DR	P-PSDB; ABB77581...		
XX	PT	Human FGF23 protein mutant for lowering blood phosphorus level,		
XX	PT	applicable in gene therapy remedies for hyperphosphatemia -		
XX	PS	Disclosure; Page 44-46; 64pp; Japanese.		
XX	XX	The invention relates to a DNA (ABN81575) encoding a protein (ABB77581)		
XX	XX	FGF23 and mutants FGF23 comprising an amino acid substitution of arginine		
XX	XX	at position 176 to glutamine and/or position 179 to glutamine or		
XX	XX	tryptophan. The mutants are generated by introducing the following base		
XX	XX	changes in the nucleic acid sequence: R176Q mutant is generated by		
XX	XX	G527A; R179Q is generated by C536A; and R179W is generated by C535T. The		
XX	XX	protein and encoding DNA are applicable in remedies for		
XX	XX	hyperphosphataemia, including gene therapy.		
XX	XX	Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;		
XX	XX	Query Match 46.9%; Score 756; DB 24; Length 756;		
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.5e-172;		
XX	XX	Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
Qy	147	AT	GTGGGGGCGCCGCTCAGGCTCTGGGTCGTGCTTGTCAGACGCTTCGACAGATGACC	206

Db	1	ATGTTGGGGGGCCCGCTCAGGCTCTGGGCTGTGTGCTTGTGACACCGTCTGAGCATAGC	60
Qy	207	GTCTCTCAGAGCTTATCCCATATGCTCTCCCACTGCTCGGCTTCAGCTGAGGCTGATC	266
Db	61	GTCTCAGAGCTTATCCCATATGCTCTCCCACTGCTCGGCTTCAGCTGAGGCTGATC	120
Qy	267	CACCTGTACAGACGACGACGAGAAACAGCTACACCTGACAGATCCCAAGATGGCCAT	326
Db	121	CACCTGTACAGACGACGACGAGAAACAGCTACACCTGACAGATCCCAAGATGGCCAT	180
Qy	327	GTGATGACGACCCCATCAGACCATCTACAGTCCCTGATGATCAGATCAGAGATGCT	386
Db	181	GTGATGACGACCCCATCAGACCATCTACAGTCCCTGATGATCAGATCAGAGATGCT	240
Qy	387	GGCTTGTGTGATTTACAGGTGTGATGAGACGAGATACCTCTGATGATTTTCAGAGGC	446
Db	241	GGCTTGTGTGATTTACAGGTGTGATGAGACGAGATACCTCTGATGATTTTCAGAGGC	300
Qy	447	AACATTTTGTGATCACAATATTTGACCCCGAGAACTGACAGTTCCAAACACGACCTG	506
Db	301	AACATTTTGTGATCACAATATTTGACCCCGAGAACTGACAGTTCCAAACACGACCTG	360
Qy	507	GAAAAACGAGTACGACGTCTACCTCTCTCAGTATCACTTCTCTGATCAGTCTGAGGCGG	566
Db	361	GAAAAACGAGTACGACGTCTACCTCTCTCAGTATCACTTCTCTGATCAGTCTGAGGCGG	420
Qy	567	GCGAAGAGAGCCTTCTGTGACAGGAGATGAAACCAACCCCGATCTCCAGTTCTGTCCCG	626
Db	421	GCGAAGAGAGCCTTCTGTGACAGGAGATGAAACCAACCCCGATCTCCAGTTCTGTCCCG	480
Qy	627	AGGAACGAGATCCCTCTATTTCACTTTCAACACCCCATACCAAGGCGGACACCCGAGC	686
Db	481	AGGAACGAGATCCCTCTATTTCACTTTCAACACCCCATACCAAGGCGGACACCCGAGC	540
Qy	687	GCCGAGACGACCTCGAAGCGGGAACCCCTGTGAAGCTGAAGCCCGGCGCCGAGTATAC	746
Db	541	GCCGAGACGACCTCGAAGCGGGAACCCCTGTGAAGCTGAAGCCCGGCGCCGAGTATAC	600
Qy	747	CCGCCCCCGGCTCTCTTTCAAGAGACTCCGAGCCCGAGGACAAACAGCCCGATGGCC	806
Db	601	CCGCCCCCGGCTCTCTTTCAAGAGACTCCGAGCCCGAGGACAAACAGCCCGATGGCC	660
Qy	807	AGTACCCATTAGAGGAGTGTGTCAGGGGCGGTGAGTGAACAGCAGCTGTGGGGAACGGC	866
Db	661	AGTACCCATTAGAGGAGTGTGTCAGGGGCGGTGAGTGAACAGCAGCTGTGGGGAACGGC	720
Qy	867	CCGGAAGGCTGCGGCCCCCTTGCCTAATTTATCTAG	902
Db	721	CCGGAAGGCTGCGGCCCCCTTGCCTAATTTATCTAG	756

RESULT 15
 ID ABL91738 standard; DNA; 756 BP.
 ABL91738;
 28-MAY-2002 (first entry)
 Human polynucleotide SEQ ID NO 81.
 Human; HIV; HCV; gene expression; oligonucleotide; tumour; pathogen;
 Plasmidium; virus; viroid; cytokine; prion; antisense oligonucleotide;
 cytosolic; virulence; protozoicide; antibacterial; ds.
 Homo sapiens.
 DE10100586-Cl.
 11-APR-2002.
 09-JAN-2001; 2001DE-1000586.
 PF

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 11:51:21 ; Search time 2480 Seconds

(without alignments)
10527.066 Million cell updates/sec

Title: US-09-901-938-1

Sequence: 1612
1 cggcaaaaaggaggaatcc.....tgagcactctctgtctcgct 1612

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estnum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_oher:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	35.4	719	17	AG095702 Pan trogl
2	220.6	13.7	470	13	B1789859
3	212.6	13.2	433	10	BB850709
4	102.8	6.4	438	17	AA0412342
5	99.6	6.2	564	17	AA0570344
6	72.6	4.5	741	12	BB869144

7	72.6	4.5	835	12	BB869616	BE869616 601512637
8	72.6	4.5	888	13	B1919047	B1919047 603180811
9	68.4	4.2	950	11	AK007574	AK007574 Mus muscu
10	63.8	4.0	708	12	BG328684	BG328684 602427957
11	56.4	3.5	925	17	CNS0091P	AL053013 Drosophi1
12	54	3.3	1201	17	CNS016A0	AL106482 Drosophi1
13	53.6	3.3	206	10	AM395897	AL095897 sh07B05.Y
14	53.4	3.3	889	17	CNS006MT	AL065765 Drosophi1
15	52.4	3.3	796	17	CNS0118D	AL099943 Drosophi1
16	52	3.2	1024	12	BE965125	BE965125 601658918
17	51.8	3.2	152	12	BE877210	BE877210 601485130
18	51.8	3.2	421	9	AI961371	AI961371 wt17F04.X
19	51.8	3.2	530	12	BG308044	BG308044 Im56B06.Y
20	51.8	3.2	839	17	CNS004NB	AL054280 Drosophi1
21	51.6	3.2	215	9	AI874303	AI874303 wms0h10.x
22	51.4	3.2	594	10	BB619211	BB619211 BB619211
23	51.4	3.2	600	12	BG807855	BG807855 2072-92.M
24	51.4	3.2	1017	17	CNS015K4	AL105550 Drosophi1
25	51.2	3.2	820	12	BE964506	BE964506 601658618
26	51.2	3.2	921	12	BG282532	BG282532 602406405
27	50.8	3.2	634	9	AL514497	AL514497 AL514497
28	50.8	3.1	1076	17	CNS015E0	AL106110 Drosophi1
29	50.6	3.1	1124	17	CNS073BM	AL427304 clone BAO
30	50.4	3.1	316	13	B1506901	B1506901 B170029A
31	50.4	3.1	319	9	AA814555	AA814555 of42f07.s
32	50.4	3.1	339	9	AI590021	AI590021 tr74h11.x
33	50.4	3.1	653	12	BG170925	BG170925 602333695
34	50.4	3.1	671	9	AL514097	AL514097 AL514097
35	50.2	3.1	119	12	BG670429	BG670429 DNBBB03
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38	50	3.1	368	9	AA828436	AA828436 cc46c05.s
39	50	3.1	440	9	AI359279	AI359279 qy27d12.x
40	50	3.1	468	9	AL514541	AL514541 AL514541
41	50	3.1	1884	12	BF530637	BF530637 602071926
42	49.8	3.1	1201	17	CNS016B1	AL106519 Drosophi1
43	49.6	3.1	322	9	AA213024	AA213024 mw86h08.x
44	49.6	3.1	399	12	BG384192	BG384192 303172.MA
45	49.4	3.1	404	9	AI860694	AI860694 w115D12.X

ALIGNMENTS

RESULT 1
AG095702 719 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-096N15.R, genomic survey sequence.
ACCESSION AG095702
VERSION AG095702.1 GI:16647544
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone lib:PTB Chimpanzee Male
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 719)
REFERENCE Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22, Suenro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpes@sc.riken.go.jp, URL:http://hsp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the Rad process and may have higher chance of clone tracking errors.

PRIMERS Sequencing: M13Rev LIBRARY Vector : pKS145 R.Site 1 : SacI R.Site 2 : SacI

FEATURES Source Location/Qualifiers

1..719
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-096N15.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC library"
BASE COUNT 171 a 194 c 175 g 177 t 2 others
ORIGIN

Query Match 35.4%; Score 571; DB 17; Length 719;
Best Local Similarity 93.0%; Pred. No. 3.5e-89;
Matches 613; Conservative 0; Mismatches 35; Indels 11; Gaps 1;

QY 749 GAGCCGCGCTCTGTTCAAGAGAGTCCCGAGCGCGGAGCAACAGCCGATGGCCAG 808
DB 70 GAGCCGCGCTCTGTTCAAGAGAGTCCCGAGCGCGGAGCAACAGCCGATGGCCAG 129
QY 809 TGACCCATTAGGGGTGTGTCAGGGGCGGTGAGTGAACAAGCAGCTGGGGAACGGGCC 868
DB 130 TGACCCATTAGGGGTGTGTCAGGGGCGGTGAGTGAACAAGCAGCTGGGGAACGGGCC 189
QY 869 GGAAGGCTGCGCGCCCTTCCCAAGTTCATCTAGGGTCTGCTGGAAGGCAACCTCTTTAA 928
DB 190 GGAAGGCTGCGCGCCCTTCCCAAGTTCATCTAGGGTCTGCTGGAAGGCAACCTCTTTAA 249
QY 929 CCATCCCTCAGCAACAGAGCTTCCCAAGAGCAAGGTCCTTGAAGTCCGAGAGAG 988
DB 250 CCATCCCTCAGCAACAGAGCTTCCCAAGAGCAAGGTCCTTGAAGTCCGAGAGAG 309
QY 989 GGAAGGCTGCGCGCGGTGTGTAAGATTTGCTGCTTCTGCGGCTCTTCCAGAGAG 1048
DB 310 GGAAGGCTGCGCGCGGTGTGTAAGATTTGCTGCTTCTGCGGCTCTTCCAGAGAG 369
QY 1049 GTCTCTGTAAGCAACAGCTTTAGGCGCCAGTCAAGGGGTTTACCGCTTCTCACTCC 1108
DB 370 GTCTCTGTAAGCAACAGCTTTAGGCGCCAGTCAAGGGGTTTACCGCTTCTCACTCC 429
QY 1109 ATATGAACACCTTCCCAATAGAAACCCCAAGGTAACTAAGAAATTTCCCTTCAAT 1168
DB 430 ATATGAACACCTTCCCAATAGAAACCCCAAGGTAACTAAGAAATTTCCCTTCAAT 489
QY 1169 GAAGGTAGAGAGAGGGGTCTCTCCCAATATTTCTTCTGCTCTCTCTCTTAA 1228
DB 490 GAAGGTAGAGAGAGGGGTCTCTCCCAATATTTCTTCTGCTCTCTCTCTTAA 549
QY 1229 TCACCTTTAAGATATAAAAAAAAAAAAAAAAAAAAAAAAAAGAGTGGGTCTCTG 1288
DB 550 TCACCTTTAAGATATAAAAAAAAAAAAAAAAAAAAAAAAAAGAGTGGGTCTCTG 598
QY 1289 AGCTTAAGCTTTGAAGGTGTAGGGAAGGAATTCGAGATCCCAAGAGCTTCTCACT 1348
DB 599 AGCTTAAGCTTTGAAGGTGTAGGGAAGGAATTCGAGATCCCAAGAGCTTCTCACT 658
QY 1349 GGCCTATGATTTATGATGATGCCCCGATGCCAGCTGGAGTTGAGTGGCAACCTTG 1407
DB 659 GGCCTATGATTTATGATGATGCCCCGATGCCAGCTGGAGTTGAGTGGCAACCTTG 717

RESULT 2
LOCUS B1789859 470 bp mRNA linear EST 12-MAR-2002
DEFINITION ic4d412.y1 Melton Normalized Mixed Mouse Pancreas 1 NI-MMSI Mus
ACCESSION B1789859
VERSION B1789859.1 GI:15817584

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE
JOURNAL
COMMENT
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
1 (bases 1 to 470)
Melton,D., Brown,J., Keny,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scaer,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisstein,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@molp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:1942717 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from GIBCO
High quality sequence stop: 458.

FEATURES Source

1..470
/organism="Mus musculus"
/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5656391"
/clone_lib="Melton Normalized Mixed Mouse Pancreas 1
NI-MMSI"
/sex="Both for embryonic & newborn, male for adult and
adult islet"
/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
adult, mixed"
/lab_host="DH10B"
/note="Vector: pSPORT1, Site 1: Not I; Site 2: Sal I; Five
libraries representing E10.5/12.5 pancreatic bud, E16.5
pancreas, newborn pancreas, adult pancreas, and adult
islets of Langerhans were separately constructed using
Superscript Plasmid Library kit (Life Technologies). cDNA
was made by oligo-dt priming and size-selected by column
fractionation. Libraries were amplified once on solid
support and plasmid DNA from each library was prepared
and mixed in equal amounts. The mixed library DNA was
normalized by method #4 from Bonaldo, Lennon, and Soares
1996 Genome Research 6:791-806; 0.5 microgram
5 micrograms PCR product representing mixed library
inserts and hybridized to an Ecot of 6. Single-stranded
(unhybridized) plasmids were isolated by hydroxyapatite
chromatography and used to make this library."
BASE COUNT 75 a 166 c 139 g 89 t 1 others
ORIGIN

Query Match 13.7%; Score 220.6; DB 13; Length 470;
Best Local Similarity 69.0%; Pred. No. 1.5e-28;
Matches 301; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 466 ATTTCAGCCGAGAGATGAGGTTCCACACGAGAGCTGGAAAGGGTACAGCTCT 525
DB 35 ACTTCAGCCGAGAGATGAGGTTCCGAGAGAGCTGGAAAGGTCTATATACGCTT 94
QY 526 ACCACTCTCCCTAGTATCACTTCTGTGATGTGGCCGGGCGGAGAGAGCTTCCTGC 585
DB 95 ACTTGTGAGAGATCATCTACTGTGAGCTTGGGCGGCGGCGGAGAGGATTTCCAGC 154

Qy	586	CAGGACATGAACCCACCCCGGATCCGAGTTCCTGTCGAGAGAAAGAGATCCCTTAA	645
Db	155	CGGGACCAACCCGCGCCCTTCTCCAGTTCCTGGGCGCAGAGAAAGAGATCCCGCTGC	214
Qy	646	TTCACTTCAACACCCCATATCCAAGCGGGACACCCGAGAGCGCAGAGAGACTCGGAGC	705
Db	215	TGTTCCTTCAACACTGTTCGCGCCACGGGCGCACAGCCGACGGCCGAGAGATCCACCCGAGC	274
Qy	706	GGGACCCCTTGAACTGTGTGAAGCCCGGGCCCGGATGACCCCGGCCCCGGGCTCTGT	765
Db	275	GGACCCCACTGAACGTGTCAAGCCGCGGGCCCGCGCAGCCTGTGCTCTGTATCTGCT	334
Qy	766	CACAGAGCTCCCGAGCGCCGAGACACAGCCCGATGGCAGTGAACCATTAAGGGGTGG	825
Db	335	CTCGCAGCTGCCGAGCGCAGAGAAAGTGGCCCCCGACGACAGATCTCTGGGGGTGC	394
Qy	826	TCAAGGGCGGTTCGAGTGAACACGCAAGCTGTGGGGGAAAGGGCCCGGAAAGCTCGCGCCCT	885
Db	395	TGCGCAGAGGCGCTTGAGATGTCTCGGGGGGCGCGGAGGCGCGGATAGGTGTGCGCCCT	454
Qy	886	TGCGCAAGTTCATCTA	901
Db	455	TTCCCAAGTTCTCTA	470

RESULT 3	LOCUS	DEFINITION	ACCESSTION
BB850709	BB850709	433 bp mRNA linear EST 26-NOV-2001	
	BB850709	RIKEN full-length enriched, adult inner ear Mus musculus	
	CDNA clone F930108M5 5', mRNA sequence.		
	BB850709		

```
REVISION BB850709
VERSION BB850709.1
KEYWORDS GI:17092163
DOT
```

SOURCE	house mouse.
ORGANISM	Mus musculus.

REFERENCE AUTHORS

TITLE

JOURNAL
COMMENT

Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-2 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. *Genome Res.* 10 (10), 1617-1630 (2000)
waegi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
S., Kawai, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. *Genome Res.*
10 (11), 1757-1771 (2000)
Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Y. and Hayashizaki, Y.

FEATURES
source
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2): 281-289 (2001)
Please visit our web site (<http://genome.sgc.riken.go.jp>) for
further details.
e mouse tissues.
Location/Qualifiers
1. .453

BASE COUNT	102 a	128 c	108 g	95 c
ORIGIN				

Query Match	13.2%;	Score 212.6;	DB 10;	Length 433;
Best Local Similarity	74.6%;	Pred. No. 3.6e-27;		
Matches 311; Conservative	0;	Mismatches 94;	Indels 12;	Gaps 3

39 CAGTACTTGCAGGAGAGAAAGCCAGTAAAGCCCTGGCCAGAGAGTCCGACA 98

Db 28 CAGCTTCTTCTAGGAAGAAGAAAGCCAGCAAGGCCAGCCTG-----TCTG 78

Db

79 GGAGTGTGAGTATCAATCAACTCGAGATTATGCCCTTCAGTGTATGCA--ATGCTAGGGAACC 13

159 CGCCTCAGGCTCTGGGATCTGTGCCCTTGGACAGGTCMGACACATGAGAGTTCCTCAGAGCC 21

137

[illegible]

219 TATCCCAATGCCCTCCACCTGCTGGTCC-AGCTGGGGTGGCCTGATCCACCTGTACAC 27

D5 197 TATCCAGACACTTCCCATTTGCTTGGCTCCACCTGGGGAAGCCTGACCCACCTGTACAC 25

QY 278 AGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGCCATGTGATGGCC 33

Db 257 GGCTACAGCCAGAACAGCTATCACCTACAGATCCATAGGGATGGTCATGTAGATGGCAC 31

338 ACCCCATCAGACCATCTACAGTCCCTGATGATCAGATCAGAGGATGCTGCTTTGTGT 39

Db 317 CCCCCATGACCATCTACAGTGCCTGATGATTACATCAGAGGACGCCGCTCTGTGGT 37

398 GATTACAGGTCGATGAGCAGAAATACCTCTGCATGCAATTTCAGAGGCAACATTTT 454

Db 377 GATACAGCAGCCATGACTCGAAGTTCTTTGTATGATCTTCCACCGCAACATTTT 433

[illegible]

RESULT 4

LOCUS	438 bp	DNA	Linear	GSS 23-MAR
AQ412342				

DEFINITION	REFERENCE
RPC1-11-177D20.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-177D20.TJ, DNA sequence.	1

ACCESSION	AQ412342
VERSION	AQ412342.1
	GI:4471830

KEYWORDS
GSS.
SOURCE
human.

ORGANISM Homo sapiens
Fukuyama's Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Primates: Hominidae: Homo

1 (bases 1 to 400)
Mammalia; Eutheria;
Primates; Homini-
daae; Homo.

AUTHORS
1 (cases 1 LO 438)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venturi, A.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPCI-11-177D20.TV
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: SP6
 Class: BAC ends.
FEATURES
 source
 1. .438
 /organism="Homo sapiens"
 /db_xref="GDB:7567675"
 /db_xref="taxon:9606"
 /clone="RPCI-11-177D20"
 /clone_1b="RPCI-11"
 /sex="Male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 123 a 73 c 116 g 126 t
ORIGIN

Query Match 6.4%; Score 102.8; DB 17; Length 438;
 Best Local Similarity 79.2%; Pred. No. 3.4e-08;
 Matches 122; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 317 GAATGGCATGTGGATGGCGACCCCATCAGACCATCTACAGTCCCTGATGATCATGTC 376
 DB 213 GGAATGGCAATGAGCTTTGGCCCTGCTGTTTTCATATGTCCTGATGATCATGTC 272

QY 377 AGAGAGTCTGGCTTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTCTGCATGGA 436
 DB 273 AGAGAGTCTGGCTTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTCTGCATGGA 332

QY 437 TTTCAGAGGCAACATTTTGGATCACAATTTTC 470
 DB 333 TTTCAGATGCAACATTTTGGATCATTGAGTTTC 366

RESULT 5
 AOS70344 564 bp DNA linear GSS 01-JUN-1999
 LOCUS HS_5352.B1.G09.T7A.RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=928 Col=17 Row=N, DNA sequence.
 ACCESSION AOS70344
 VERSION AOS70344.1 GI:4963564
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 564)
REFERENCE Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
AUTHORS Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
TITLE Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
 Plate: 928 row: N column: 17
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 564.
FEATURES
 source
 1. .564
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=928 Col=17 Row=N"
 /clone_1b="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
BASE COUNT 152 a 100 c 138 g 169 t 5 others
ORIGIN

Query Match 6.2%; Score 99.6; DB 17; Length 564;
 Best Local Similarity 77.9%; Pred. No. 1.1e-07;
 Matches 120; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 317 GAATGGCATGTGGATGGCGACCCCATCAGACCATCTACAGTCCCTGATGATCATGTC 376
 DB 244 GGAATGGCAATGAGCTTTGGCCCTGCTGTTTTCATATGTCCTGATGATCATGTC 303

QY 377 AGAGAGTCTGGCTTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTCTGCATGGA 436
 DB 304 AGAGAGTCTGGCTTTGTGTGATTAACAGGTGTGATGAGAGAAATACCTCTGCATGGA 363

QY 437 TTTCAGAGGCAACATTTTGGATCACAATTTTC 470
 DB 364 TTTCAGATGCAACATTTTGGATCATTGAGTTTC 397

RESULT 6
 BE869144 741 bp mRNA linear EST 20-OCT-2000
 LOCUS BE869144
 DEFINITION 601445130P1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849343 5', mRNA sequence.
 ACCESSION BE869144
 VERSION BE869144.1 GI:10317920
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 741)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
 DNA Sequencing by: MGC Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: http://image.llnl.gov
 Plate: LILN9566 row: k column: 08
 High quality sequence stop: 696.

FEATURES

source

Location/Qualifiers
1. 741
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3849343"
/tissue_type="NIH MGC_65"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: PCMV-SPORE; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies." 259 c 235 g 125 t

BASE COUNT

122 a 259 c 235 g 125 t

ORIGIN

Query Match

Best Local Similarity 53.8%; Pred. No. 0.0048;
Matches 150; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 293 CAGCTACCACTGAGATCCAGAAATGGCCATGTGATGGCCACCCCATCAGACCAT 352
DB 277 CAGCTGCTTCTGCGATCCGTCGCGACGGGCTGTGATGCGCGGGCCAGACGC 336
QY 353 CTACAGTGCCTGATGATCAGATGAGATGCTGCTTTGTGTATTAAGGTGTGAT 412
DB 337 GCACAGTTTCTGAGATCAAGGACATGCTCTGCGACCGTGCATCAAGGCGTGCA 396
QY 413 GACGAGAACTGACTCTGATGATTTCAAGGCAACATTTTGGATCACTATTTCGA 472
DB 397 CACGTCGGGTACTCTGATGAGGCGCGACGCGAATGCAAGGCGCTGCTTCAGTCTC 456
QY 473 CCGGAGAACTGAGGTTCCACACACGATGGAAGGATGACGCTTACCACTC 532
DB 457 GGAGGAAGACTGTGCTTTCAGAGAGAGATCCGCCAGATGCTCAATGTACCATC 516
QY 533 TCCTCAGTACTCTCTGCTGATGCTGGCGCGCGCA 571
DB 517 CGAGAGACACCGCTCCGGTCTCCGAGACAGTGC 555

RESULT 7

BE889616

LOCUS

601512637F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:391492 5',
835 bp mRNA linear EST 20-OCT-2000
DEFINITION

ACCESSION

BE889616

EST.

VERSION BE889616.1 GI:10347118
KEYWORDS

SOURCE

human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM9735 row: 1 column: 09

High quality sequence stop: 687.

FEATURES

source

Location/Qualifiers
1. 835
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:391492"
/clone_lib="NIH_MGC_71"

BASE COUNT

139 a 284 c 267 g 145 t

ORIGIN

Query Match
Best Local Similarity 53.8%; Pred. No. 0.0046;
Matches 150; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 293 CAGCTACCACTGAGATCCAGAAATGGCCATGTGATGGCCACCCCATCAGACCAT 352
DB 285 CAGCTGCTTCTGCGATCCGTCGCGACGGGCTGTGATGCGCGGGCCAGACGC 344
QY 353 CTACAGTGCCTGATGATCAGATGAGATGCTGCTTTGTGTATTAAGGTGTGAT 412
DB 345 GCACAGTTTCTGAGATCAAGGACATGCTCTGCGACCGTGCATCAAGGCGTGCA 404
QY 413 GACGAGAACTGACTCTGATGATTTCAAGGCAACATTTTGGATCACTATTTCGA 472
DB 405 CACGTCGGGTACTCTGATGAGGCGCGACGCGAATGCAAGGCGCTGCTTACGATC 464
QY 473 CCGGAGAACTGAGGTTCCACACACGATGGAAGGATGACGCTTACCACTC 532
DB 465 GGAGGAAGACTGTGCTTTCAGAGAGAGATCCGCCAGATGCTCAATGTACCATC 524
QY 533 TCCTCAGTACTCTCTGCTGATGCTGGCGCGCGCA 571
DB 525 CGAGAGACACCGCTCCGGTCTCCGAGACAGTGC 563

RESULT 8

B1919047

LOCUS

603180811F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245034 5',
888 bp mRNA linear EST 17-OCT-2001
DEFINITION

ACCESSION

B1919047

EST.

VERSION B1919047.1 GI:16200101
KEYWORDS

SOURCE

human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM1618 row: e column: 03

High quality sequence stop: 833.

FEATURES

source

Location/Qualifiers
1. 888
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/db_xref="taxon:9606"
/clone="IMAGE:5245034"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Organ: brain; Vector: PCMV-SPORE; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

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/dev_stage="10 day old"
1.950
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185.817
/gene="Pgf21"
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evidence:ISS
fibroblast growth factor 21
putative"
/codon_start=1
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/db_xref="GI:12841203"
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GPRFLPMGLHPEPODQAGFLPPRPDVSSDPLSMVEPLQGRSPSYAS"

BASE COUNT 204 a 278 c 241 g 227 t

ORIGIN

Query Match
Best Local Similarity 53.8%; Score 68.4; DB 11; Length 950;
Matches 141; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 299 CCACCTGCAGATCCACAAGATGGCCATGTGATGGCGCACCCCATAGACCATTAAG 358
DB 364 CCACCTGCAGATAGGAGATGAAACAGTGTAGGCGCACACCGCATCCAGAAAG 423
QY 359 TSCCTGATGATCAGATCAGAGATGCTGTGTGATTAAGAGTGTGATGAGCAG 418
DB 424 TCTCCTGAGCTCAAGACCTGAAAGCGGATCATTAATCTGGGTCTCAAGCTTC 483
QY 419 AAGATACCTGTGATGATTTAGAGGCAACATTTTGTATCACTATTTCACCGGA 478
DB 484 TAGGTTCTTTGCAACAGCAGATGAGCTCTATGATCGCTTCACTTTGATCTGA 543
QY 479 GAATGCAGATTCACACACAGCGTGGAAACGGGTACGAGTCTACCTCTCTCA 558
DB 544 GGCCTGCACCTTGAAGAACTGCTGTGAGAGCGGTTCAAATGTATACGATGTAAGC 603
QY 539 GTATCACTTCTGTGATCTG 560
DB 604 CCATGGCTTCCCTGCTCTG 625

RESULT 10
BG328684 708 bp mRNA linear EST 27-FEB-2001
LOCUS BG328684
DEFINITION 602427857p1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4547223 5',
mRNA sequence.
ACCESSION BG328684
VERSION BG328684.1 GI:1135122
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 708)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: LNCM1235 row: a column: 16
High quality sequence stop: 708.

FEATURES

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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4547223"
/clone_1lb="NIH MGC_15"
/ribseq_type="a9enocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAACAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 115 a 247 c 227 g 119 t

ORIGIN

Query Match
Best Local Similarity 52.9%; Score 63.8; DB 12; Length 708;
Matches 137; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 293 CACTTACCACTTCAGATCCACAAGATGGCCATGTGATGGCGCACCCCATAGACCAT 352
DB 305 CACTCTCTTCTCGGATCCGTCACGCGCTGTGAGCTGCGCGCGGCGCAGAGCGC 364
QY 353 CTACAGTGCCTGATGATCAGATCAGAGATGCTGTGTGATTAAGAGTGTGAT 412
DB 365 GCACATTTGCTGAGATCAAGCACTGCTGTGCGACCGTGGCCATCAAGGCGTGA 424
QY 413 GAGCAGAAATACCTTGATGATTTAGAGCAACATTTTGTATCACTATTTCGA 472
DB 425 CAGCGTGGCTGATCTGTGATGGCGCCGCAAGATGACAGGGCTGCTTACGATC 484
QY 473 CCGGGAATCTGAGTTCAACACAGCGTGGAAACGGGTACGAGCTTACCATC 532
DB 485 GGAGGAAGACTGTGCTTTCAGAGAGAGATCCGCCAGATGCTTACATGATGACGATC 544
QY 533 TCTCTGATTCATCTTCG 551
DB 545 CGAAGACACCGCTCCCG 563

RESULT 11
CNS0091P/C 925 bp DNA linear GSS 03-JUN-1999
LOCUS CNS0091P/C
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL053013
VERSION AL053013.1 GI:4934461
KEYWORDS GSS.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Empidoidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Osoegawa and
Aaron Mamoser in Peter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial

/tissue_type="Immature flowers of field grown plants"
 /lab_host="Xl10-Gold"
 /note="vector: pBluescript II XR; Site 1: EcoRI; Site 2:
 XhoI. This cDNA library was constructed from mRNA isolated
 from immature flowers of field grown plants. The cDNA
 library was prepared using the Stratagene pBluescript II
 XR library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a poly
 (dT) sequence with a XhoI restriction site. EcoRI adapters
 were ligated to the blunt-ended cDNA fragments followed by
 XhoI digestion. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into Xl10-Gold host cells. This library was
 constructed by Dr. Randy Shoemaker and Dr. John
 Breiding."

BASE COUNT 134 a 17 c 17 g 38 t
 ORIGIN

Query Match 3 %; Score 53.6; DB 10; Length 206;
 Best Local Similarity 66.4%; Pred. No. 14;
 Matches 77; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Oy 1159 TCCCTTCATGAAGTAGAGAGAGGGGCTCTCCACATATTTCTCTTCCTGGCCT 1218
 Db 19 TTCCGCTATGAAATTTGCTAAAGGGTTCAACAGTAATGTTACTCTTGATATCA 78
 Oy 1219 CTCCTTTATACATTTTAAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
 Db 79 AGCCCTCATTTTCATCTTTGAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 134

RESULT 14
 CDS006MT/c 889 bp DNA linear GSS 03-JUN-1999
 LOCUS
 DEFINITION Drosophila melanogaster genome survey sequence Tm3 and of BAC #
 BACR14K09 of RPCT-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL065765
 AL065765.1 GI:4944645
 GSS.
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydrioidae; Drosophilidae; Drosophila.
 1 (bases 1 to 889)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqdef@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuo Ooegawa and
 Aaron Mamoser in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCT-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1. 889
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone="BACR14K09"
 /clone_lib="RPCT-98"

FEATURES
 source

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Best Local Similarity	44.9%;	Pred. No. 9.5;			
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Dd	478	AAGTTWAAVTTTCCTCDVTWTTCYCXTMAAMATTTHSCYTTCCTCTTAACYTC	419		
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Dd	418	AACYYTWATAATTTMTTTCCTCTCATATCAAAAAAAAATTCATATTTTMTTANNA	359		
OY	1197	CATATTCTCTCTCCTGTGCCTCCTCTTATCATCTTTTAAGCATATAAAAAAAAA	1256		
Dd	358	TTTTATTTTATCTTCTCHYYMATWAAAYMAACAIPAAAAANAANAANAANAANA	299		
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Dd	298	AAAAAAAAAAAAAAAAAAAA 281			
RESULT 15					
CNS0118D/c					
LOCUS	CNS0118D 796 bp DNA linear GSS 26-Jul-1999				
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC				
SOURCE	BACN05J08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL099943				
VERSION	AL099943.1 GI:5611554				
KEYWORDS	GSS.				
ORGANISM	Drosophila melanogaster.				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridioidea; Drosophilidae; Drosophila.				
AUTHORS	1 (bases 1 to 796)				
TITLE	Genoscope.				
JOURNAL	Direct Submission				
COMMENT	Submitted (23-Jul-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seget@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbeloBAC11.				
FEATURES					
Source	Location/Qualifiers 1..796 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone="BACN05J08" /clone_1kb="DrosBAC" /plasmid="pbeloBAC11" /note="end : T7"				
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Best Local Similarity	29.6%;	Pred. No. 15;			
Matches	58;	Conservative	66;	Mismatches	72; Indels 0; Gaps 0
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Dd	701	SBCCCKGKCKSCCCCCCTCTCMCCCCTCCMKCKCYTMGKTHTMMKMYMCKMMKKCK	642		
OY	1139	CAACAGGTAACTAGAAATTTCCCTTCATGAGAGTAGAGAGAGGGGTCTCTCCACA	1198		

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Db      641 KMMKGMAMMMRRMKGTSTMCSCGTMYKMMMMMAAAMGTBASTMYMTMCMCKEC 582
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Db      581 YCMGGAAMKISTIGHKMTMMMAAAMMKTTCTMMAAAAAAAMKAAAAA 522
Qy      1259 AAAAAAAAAAAAAA 1274
Db      521 AAAAAAAAAAAAAA 506

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Search completed: May 28, 2003, 14:14:08
 Job time : 2498 secs

GenCore version 5.1.4 p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 21:20:14 ; Search time 256 Seconds

(Without alignments)
8314.786 Million cell updates/sec

Title: US-09-901-938-1

Perfect score: 1612

Sequence: 1 cggcaaaaaggaggggaatcc.....tgcagcctctgtctgct 1612

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1237.4	76.8	1239	9	US-10-000-489-25
6	1211	75.1	1211	10	US-09-754-634A-1
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23	798	49.5	996	9	US-09-990-562-510	Sequence 510, App
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39	798	49.5	996	9	US-09-991-157-510	Sequence 510, App
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42	798	49.5	996	9	US-09-997-573-510	Sequence 510, App
43	798	49.5	996	9	US-10-123-262-265	Sequence 265, App
44	798	49.5	996	9	US-10-142-423-265	Sequence 265, App
45	798	49.5	996	9	US-09-990-443-510	Sequence 510, App

ALIGNMENTS

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RESULT 1
US-09-901-938-1
; Sequence 1, Application US/09901938
; Patent No. US20020156001A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/09/901,938
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-901-938-1

Query Match      100.0%; Score 1612; DB 9; Length 1612;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 661 CCATACCAAGCGGCGCAACCGGAGCGCGGAGAGAGTCTGAGAGCGGAGACCCCTGAAACG 720
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 Db 841 TGAACAGGACGCTGGGGGAGAGCGCGCGGAGAGGCTGCGCGCTTGGCCAGTTCATCT 900
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 QY 1561 ATCATATATAGAAACTAGGCTCCCTTACAGAGGTGAGACCTTGTGTCTGCT 1612
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RESULT 2
 US-09-731-872-57
 ; Sequence 57, Application US/09731872
 ; Patent No. US20020102604A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, Jean Baptiste
 ; APPLICANT: Bouguerelet, Lydie
 ; APPLICANT: Jobert, Severin
 ; TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED -PROTEINS
 ; FILE REFERENCE: 78. US3. REG
 ; CURRENT APPLICATION NUMBER: US/09/731, 872
 ; CURRENT FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,629
 ; PRIOR FILING DATE: 1999-12-08
 ; PRIOR APPLICATION NUMBER: US 60/187,470
 ; PRIOR FILING DATE: 2000-03-06
 ; NUMBER OF SEQ ID NOS: 482
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 57
 ; LENGTH: 1240
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 127..879
 ; NAME/KEY: s19_peptide
 ; LOCATION: 127..198
 ; OTHER INFORMATION: Von Heijne matrix
 ; OTHER INFORMATION: score 5.3860866264012
 ; OTHER INFORMATION: seq ALCSVCSMSVLR/YP
 US-09-731-872-57

Query Match 76.8%; Score 1238.4; DB 10; Length 1240;
 Best local similarity 99.9%; Pred. No. 0;
 Matches 1239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 AGTCTAGATCTCACAACAGCTACTTTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 80
 Db 1 AGTCTAGATCTCACAACAGCTACTTTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
 QY 81 GCCAGAGAGATCCCGACAGAGAGTGTGAGTTTAATCTCAGACCAACCACTCAGAGCAG 140
 Db 61 GCCAGAGAGATCCCGACAGAGAGTGTGAGTTTAATCTCAGACCAACCACTCAGAGCAG 120
 QY 141 GGCAGCATGTTGGGGGCGCGCTCAGAGCTGTGGGCTGTGGAGCTGTGAGCTGTGAGCAG 200
 Db 121 GGCAGCATGTTGGGGGCGCGCTCAGAGCTGTGGGCTGTGGAGCTGTGAGCTGTGAGCAG 180
 QY 201 ATGAGGCTCTCAGAGCTTATCCCAATGCTCCCACTGCTGGCTCAGCTGAGTGGGTGGC 260
 Db 181 ATGAGGCTCTCAGAGCTTATCCCAATGCTCCCACTGCTGGCTCAGCTGAGTGGGTGGC 240

QY 261 CTGATCCACCTGTAACAGCCAGCAGCAGGAAAGCTTACCACTGAGATCCAGAGAT 320
Db 241 CTGATCCACCTGTAACAGCCAGCAGCAGGAAAGCTTACCACTGAGATCCAGAGAT 300
QY 321 GGCATGATGATGAGGAGCAGCCCATCAGACCATCTAGTGCCCTGAGATCAGATCAGAG 380
Db 301 GGCATGATGATGAGGAGCAGCCCATCAGACCATCTAGTGCCCTGAGATCAGATCAGAG 360
QY 381 GATGCTGCTTTGATGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 440
Db 361 GATGCTGCTTTGATGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 441 AGAGGCAACATTTTGGATACACTATTTGACCCGAGAACTGACAGTTCCAAACACAG 500
Db 421 AGAGGCAACATTTTGGATACACTATTTGACCCGAGAACTGACAGTTCCAAACACAG 480
QY 501 AGCTGGAAGAGGATACAGAGCTTACCTCTCAGATGATGATGATGATGATGATGATGAT 560
Db 481 AGCTGGAAGAGGATACAGAGCTTACCTCTCAGATGATGATGATGATGATGATGATGAT 540
QY 561 GGCAGGAG 620
Db 541 GGCAGGAG 600
QY 621 TCCCGAG 680
Db 601 TCCCGAG 660
QY 681 CGAGAGGAG 740
Db 661 CGAGAGGAG 720
QY 741 ATGAG 800
Db 721 ATGAG 780
QY 801 ATGAG 860
Db 781 ATGAG 840
QY 861 AGGAG 920
Db 841 AGGAG 900
QY 921 CTCTTAAACCATCTCTCAG 980
Db 901 CTCTTAAACCATCTCTCAG 960
QY 981 CGAG 1040
Db 961 CGAG 1020
QY 1041 CACAG 1100
Db 1021 CACAG 1080
QY 1101 CTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1160
Db 1081 CTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1161 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1220
Db 1141 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1221 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 CCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1240

RESULT 3
US-09-924-340-25
; Sequence 25, Application US/09924340
; Publication No. US20030027248A1

GENERAL INFORMATION:
; APPLICANT: Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91 US2 REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 25
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..126
; NAME/KEY: CDS
; LOCATION: 127..879
; NAME/KEY: 3'UTR
; LOCATION: 880..1239
; NAME/KEY: polyA site
; LOCATION: 1224..1239
US-09-924-340-25

Query Match 76.8%; Score 1237.4; DB 9; Length 1239;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 AGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 80
Db 1 AGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 81 GCCAG 140
Db 61 GCCAG 120
QY 141 GGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 200
Db 121 GGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 201 ATGAG 260
Db 181 ATGAG 240
QY 261 CTGATCCACCTGTAACAGCCAGCAGCAGGAAAGCTTACCACTGAGATCCAGAGAT 320
Db 241 CTGATCCACCTGTAACAGCCAGCAGCAGGAAAGCTTACCACTGAGATCCAGAGAT 300
QY 321 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 380
Db 301 GGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 381 GATGCTGCTTTGATGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 440
Db 361 GATGCTGCTTTGATGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 441 AGAGGCAACATTTTGGATACACTATTTGACCCGAGAACTGACAGTTCCAAACACAG 500
Db 421 AGAGGCAACATTTTGGATACACTATTTGACCCGAGAACTGACAGTTCCAAACACAG 480
QY 501 AGCTGGAAGAGGATACAGAGCTTACCTCTCAGATGATGATGATGATGATGATGATGAT 560
Db 481 AGCTGGAAGAGGATACAGAGCTTACCTCTCAGATGATGATGATGATGATGATGATGAT 540
QY 561 GGCAGGAG 620

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Db 541 GGGGGGGAAGAGAGCTTCCTGACAGCAAGAACCCACCCCTACTCTCCAGTTCTG 600
Qy 621 TCCGGAAGAAAGAGATCCCTTAATTCATTCAACACCCCAATACAGCGGCGACACC 680
Db 601 TCCGGAAGAAAGAGATCCCTTAATTCATTCAACACCCCAATACAGCGGCGACACC 660
Qy 681 CGAGGCGCGAAGAGAGCTCGAGCGGAGCCCTCTGAACGTGTGAAGCCCGGCGCGG 740
Db 661 CGAGGCGCGAAGAGAGCTCGAGCGGAGCCCTCTGAACGTGTGAAGCCCGGCGCGG 720
Qy 741 ATGACCCCGCGCGCGCTCTGTTCACAGAGCTCCGAGCGCGGAGCAACAGCCCG 800
Db 721 ATGACCCCGCGCGCGCTCTGTTCACAGAGCTCCGAGCGCGGAGCAACAGCCCG 780
Qy 801 ATGACAGATGACCCATTAGGGGTGTGTCAGGGGCGGTGAGTGAACAGCAGCTGGGGGA 860
Db 781 ATGACAGATGACCCATTAGGGGTGTGTCAGGGGCGGTGAGTGAACAGCAGCTGGGGGA 840
Qy 861 ACAGGCGCGAAGAGCTGCGCCCTTCGCAAGTTCAATCTAGGGTGTGAGAGGCGAC 920
Db 841 ACAGGCGCGAAGAGCTGCGCCCTTCGCAAGTTCAATCTAGGGTGTGAGAGGCGAC 900
Qy 921 CTCTTTAACCATCTCTCAGCAAAAGCAGCTCTTCCAGAGACAGAGTCCCTTGAAGTT 980
Db 901 CTCTTTAACCATCTCTCAGCAAAAGCAGCTCTTCCAGAGACAGAGTCCCTTGAAGTT 960
Qy 981 CGAGATGGGAAAGGTACAGGGGCGATGTATGAAATTTGCTCTCTGGGGTCCCTTC 1040
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Qy 1041 CACAGAGGTCTGTGAGAACCAACTTTGAGGCGCAAGTATGAGGGTTTCAAGCGCTTC 1100
Db 1021 CACAGAGGTCTGTGAGAACCAACTTTGAGGCGCAAGTATGAGGGTTTCAAGCGCTTC 1080
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Db 1081 CTCACTCATATGAAACAACCTTTCCATAGAGAAACCCCAACAGGTAACTGAAGTTTC 1140
Qy 1161 CCCTCATGAGGTAGAGAGAGGGGTCTCCCAACATATTTCTCTCTGGGCTTC 1220
Db 1141 CCCTCATGAGGTAGAGAGGGGTCTCCCAACATATTTCTCTCTGGGCTTC 1200
Qy 1221 CCTCTTATCATCTTTAAGCATAAAAA 1259
Db 1201 CCTCTTATCATCTTTAAGCATAAAAA 1239

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RESULT 4
US-09-992-600A-25

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/ Sequence 25, Application US/09992600A
/ Publication No. US20030027161A1
/ GENERAL INFORMATION:
/ APPLICANT: Benjamin, Stephanie
/ APPLICANT: Tanaka, Hiroaki
/ TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
/ FILE REFERENCE: 91. US4. DIV
/ CURRENT APPLICATION NUMBER: US/09/992,600A
/ CURRENT FILING DATE: 2001-11-13
/ PRIOR APPLICATION NUMBER: US 09/924,340
/ PRIOR FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: PCT/IB01/01715
/ PRIOR FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: US 60/305,456
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/302,277
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/298,698
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: US 60/293,574
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: Jpatent

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/ SEQ ID NO 25
/ LENGTH: 1239
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: 5' UTR
/ LOCATION: 1..126
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 127..879
/ FEATURE:
/ NAME/KEY: 3' UTR
/ LOCATION: 880..1239
/ FEATURE:
/ NAME/KEY: polyA site
/ LOCATION: 1224..1239
/ US-09-992-600A-25

Query Match          76.8%; Score 1237.4; DB 9; Length 1239;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1238; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 AGCTAGATCTTCACACAGCTAATTGCAAGGAGAGAGAAAGGCCAGTAAGCCTTG 80
Db 1 AGCTAGATCTTCACACAGCTAATTGCAAGGAGAGAGAAAGGCCAGTAAGCCTTG 60
Qy 81 GCCAGAGAGTCCCGACAGAGAGTGTCAAGTTTCAATCTGACACAGCCACTCAGAGCAG 140
Db 61 GCCAGAGAGTCCCGACAGAGAGTGTCAAGTTTCAATCTGACACAGCCACTCAGAGCAG 120
Qy 141 GGCACGATGTTGGGGGGCGCGCTCAGGCTCTGGGTTGTGTCCTTGTGACAGGTCTGAGC 200
Db 121 GGCACGATGTTGGGGGGCGCGCTCAGGCTCTGGGTTGTGTCCTTGTGACAGGTCTGAGC 180
Qy 201 ATGAGCGTCTCAAGAGCTATCCCAATGCTCTCCCACTGCTCGGCTCAGCTGGGGTGC 260
Db 181 ATGAGCGTCTCAAGAGCTATCCCAATGCTCTCCCACTGCTCGGCTCAGCTGGGGTGC 240
Qy 261 CTGATCCACTGTATACACAGCACAGCCAGAGAACGTAACCACTGCGAGATCCACAGAT 320
Db 241 CTGATCCACTGTATACACAGCACAGCCAGAGAACGTAACCACTGCGAGATCCACAGAT 300
Qy 321 GGCATATGATGAGGCGGACCCCATCAGACCATCTACAGTCCCTGATGATCAATATTCAG 380
Db 301 GGCATATGATGAGGCGGACCCCATCAGACCATCTACAGTCCCTGATGATCAATATTCAG 360
Qy 381 GATGCTGGCTTTGTGTGATTAACAGTGTGATGAGCAAGATACCTCTCATGATTTTC 440
Db 361 GATGCTGGCTTTGTGTGATTAACAGTGTGATGAGCAAGATACCTCTCATGATTTTC 420
Qy 441 AGAGGCAACATTTTGGATCACTAATTTGACCCGAGAACTGCAAGTTTCAACACAG 500
Db 421 AGAGGCAACATTTTGGATCACTAATTTGACCCGAGAACTGCAAGTTTCAACACAG 480
Qy 501 ACCGTGAAAACGGGTACAGACGCTTACCACTCTCTCAATCACTTCTCTGTCAGTCTG 560
Db 481 ACCGTGAAAACGGGTACAGACGCTTACCACTCTCTCAATCACTTCTCTGTCAGTCTG 540
Qy 561 GGCAGGCGGAGAGAGGCTTCTGCGAGGAGTAAACCCCGGAGTCCAGTCCGCTCTG 620
Db 541 GGCAGGCGGAGAGAGGCTTCTGCGAGGAGTAAACCCCGGAGTCCAGTCCGCTCTG 600
Qy 621 TCCGGAAGAAAGAGATCCCTTAATTCATTCAACACCCCAATACAGCGGCGACACC 680
Db 601 TCCGGAAGAAAGAGATCCCTTAATTCATTCAACACCCCAATACAGCGGCGACACC 660
Qy 681 CGAGGCGCGAAGAGAGCTCGAGCGGAGCCCTCTGAACGTGTGAAGCCCGGCGCGG 740
Db 661 CGAGGCGCGAAGAGAGCTCGAGCGGAGCCCTCTGAACGTGTGAAGCCCGGCGCGG 720
Qy 741 ATGACCCCGCGCGCGCTCTGTTCACAGAGCTCCGAGCGCGGAGCAACAGCCCG 800
Db 721 ATGACCCCGCGCGCGCTCTGTTCACAGAGCTCCGAGCGCGGAGCAACAGCCCG 780

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Qy	801	ATGGCAGATGACCATTAAGGGGTGTGATGGGGCGGTGATGAAACACGACGTGGGGGA	860
Db	781	ATGGCAGATGACCATTAAGGGGTGTGATGGGGCGGTGATGAAACACGACGTGGGGGA	840
Qy	861	ACGGGCCCCGAAAGGTGCGCGCCCTTGCCCAAGTCATCTAGGGTGGTGGAAAGGCACC	920
Db	841	ACGGGCCCCGAAAGGTGCGCGCCCTTGCCCAAGTCATCTAGGGTGGTGGAAAGGCACC	900
Qy	921	CTCTTAACCATCCCTCAGCAACGACGCTCTCCCAAGACCAAGTCCCTAGAGTTTC	980
Db	901	CTCTTAACCATCCCTCAGCAACGACGCTCTCCCAAGACCAAGTCCCTAGAGTTTC	960
Qy	981	CGAGGATGGGAAAGGTGACAGGGGCATGTATGAAATTGCTGCTCTCTGGGGTCCCTTC	1040
Db	961	CGAGGATGGGAAAGGTGACAGGGGCATGTATGAAATTGCTGCTCTCTGGGGTCCCTTC	1020
Qy	1041	CACAGAGAGTCTCTGTGAGAACCAACTTTTAGGCCCAAGTCATGSGGTTTCAACCGCTTC	1100
Db	1021	CACAGAGAGTCTCTGTGAGAACCAACTTTTAGGCCCAAGTCATGSGGTTTCAACCGCTTC	1080
Qy	1101	CTCACTCATATAGAACCTTTCCCAATAGGAAACCCCAACAGTAAACTAGAAATTTC	1160
Db	1081	CTCACTCATATAGAACCTTTCCCAATAGGAAACCCCAACAGTAAACTAGAAATTTC	1140
Qy	1161	CCCTTCATGAAGGTAGAGAGAAAGGGTCTCTCCCAATATTTTCTCTTCTTGTCCTTC	1220
Db	1141	CCCTTCATGAAGGTAGAGAGAAAGGGTCTCTCCCAATATTTTCTCTTCTTGTCCTTC	1200
Qy	1221	CCTCTTATGACTTTTAAAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1259
Db	1201	CCTCTTATGACTTTTAAAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1239

RESULT 5
 US-10-000-489-25
 Sequence 25, Application US/100000489
 Publication No. US20030092011A1
 GENERAL INFORMATION:
 APPLICANT: Benjann, Stephane
 APPLICANT: Tanaka, Hiroaki
 TITLE OF INVENTION: HUMAN CDMAS AND PROTEINS AND USES THEREOF
 FILE REFERENCE: 91.US6.DIV
 CURRENT APPLICATION NUMBER: US/10/000,489
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: US 09/924,340
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: PCT/IB01/01715
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: US 60/305,456
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/302,277
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/298,698
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US 60/293,574
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 112
 SOFTWARE: JPatent
 SEQ ID NO 25
 LENGTH: 1239
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: 1..126
 NAME/KEY: CDS
 LOCATION: 127..879
 NAME/KEY: 3'UTR
 LOCATION: 880..1239
 NAME/KEY: polyA_site
 LOCATION: 1224..1239
 US-10-000-489-25

[illegible]

QY 1041 CACAGAGGTCCTGTGAGAACCACTTTAGAGCCCAAGTCAAGGAGTTTCAAGCCCTTC 1100
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 QY 1101 CTCACCTCATATAGAACCACTTTCCCAATAGAGAACCCCAAGGTAACTAGAAATTC 1160
 Db 1081 CTCACCTCATATAGAACCACTTTCCCAATAGAGAACCCCAAGGTAACTAGAAATTC 1140
 QY 1161 CCCTTCATGAGAGTAGAGAGAGGGGTCTCCCAACATATTTCTCTTGTGCTCT 1220
 Db 1141 CCCTTCATGAGAGTAGAGAGAGGGGTCTCCCAACATATTTCTCTTGTGCTCT 1200
 QY 1221 CCTCTTTATCATCTTTTAAAGCATATAAAAAAAAAAAAA 1259
 Db 1201 CCTCTTTATCATCTTTTAAAGCATATAAAAAAAAAAAAA 1239

RESULT 6
 US-09-754-634A-1
 / Sequence 1, Application US/09754634A
 / Patent No. US20010044525A1
 / GENERAL INFORMATION:
 / APPLICANT: Conklin, Darrell C.
 / TITLE OF INVENTION: RGF HOMOLOG ZEPF12
 / FILE REFERENCE: 00-02
 / CURRENT APPLICATION NUMBER: US/09/754,634A
 / PRIOR FILING DATE: 2001-05-11
 / PRIOR APPLICATION NUMBER: US 60/174,582
 / NUMBER OF SEQ ID NOS: 6
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 1
 / LENGTH: 1211
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (115)...(870)
 / US-09-754-634A-1

Query Match 75.1%; Score 1211; DB 10; Length 1211;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 TCACACAGGCTACTTGGCAAGGAGAGAAAGGCGAGTAAAGCGCCAGAGAGTC 92
 Db 1 TCACACAGGCTACTTGGCAAGGAGAGAAAGGCGAGTAAAGCGCCAGAGAGTC 60
 QY 93 CCGACAGAGAGTGTCAAGTTTCAATCTGACACAGCACTCAGACAGGAGCAGATGTTG 152
 Db 61 CCGACAGAGAGTGTCAAGTTTCAATCTGACACAGCACTCAGACAGGAGCAGATGTTG 120
 QY 153 GGGGCCCCGCTCAGGCTCTGGGTCTGTGCTTGTGCAAGCGTCTGACAGATGAGCGTCTC 212
 Db 121 GGGGCCCCGCTCAGGCTCTGGGTCTGTGCTTGTGCAAGCGTCTGACAGATGAGCGTCTC 180
 QY 213 AGAGCCTATCCCAATGCTCCCACTGCTGGGCTCCAGCTGGGGTGGCTGATCCACTG 272
 Db 181 AGAGCCTATCCCAATGCTCCCACTGCTGGGCTCCAGCTGGGGTGGCTGATCCACTG 240
 QY 273 TACACAGCCACAGCCAGAAAGCTTACCACTGAGATCCACAGAAATGGCCATGTGAT 332
 Db 241 TACACAGCCACAGCCAGAAAGCTTACCACTGAGATCCACAGAAATGGCCATGTGAT 300
 QY 333 GGGCAGCCCATCATGACATCTTACAGTCCCTGATGATCATGATGAGATGCTGCTTT 392
 Db 301 GGGCAGCCCATCATGACATCTTACAGTCCCTGATGATCATGATGAGATGCTGCTTT 360
 QY 393 GTGGTATTTACAGGTGTGATGAGAGAAAGTACTCTTGCATGATTTTCAAGGCAATT 452
 Db 361 GTGGTATTTACAGGTGTGATGAGAGAAAGTACTCTTGCATGATTTTCAAGGCAATT 420
 QY 453 TTGGATCACACTATTTCAGACCCGAGAACTGAGGTTCCAAACACAGAGCGCTGAAAC 512

Db 421 TTGGATCACACTATTTCGACCCGAGAACTGACAGTTTCAACACAGAGCTGGAAC 480
 QY 513 GGGTACAGCTTACCACTCTCCCTCACTATCACTTCTGGTCACTTGGGCGGCGAG 572
 Db 481 GGGTACAGCTTACCACTCTCTCTCACTATCACTTCTGGTCACTTGGGCGGCGAG 540
 QY 573 AGACCTTCTGCGAGGAGTAAACCCACCCCGTACTCCAGTTCTGTCCGAGAGAC 632
 Db 541 AGACCTTCTGCGAGGAGTAAACCCACCCCGTACTCCAGTTCTGTCCGAGAGAC 600
 QY 633 GAGATCCCCCTTAATTCATTCAACACCCCAATACAGGAGGAGACCCGAGCGGAG 692
 Db 601 GAGATCCCCCTTAATTCATTCAACACCCCAATACAGGAGGAGACCCGAGCGGAG 660
 QY 693 GAGACTCGAGAGGAGGAGCCCTGAACTGTGTAAGCCCGGAGCGGAGTGAACCCGAGCC 752
 Db 661 GAGACTCGAGAGGAGGAGCCCTGAACTGTGTAAGCCCGGAGCGGAGTGAACCCGAGCC 720
 QY 753 CCGGCTCTGTTCACAGAGCTCCCGAGCGGAGGAGCAACAGCCGATGAGCGAGTAC 812
 Db 721 CCGGCTCTGTTCACAGAGCTCCCGAGCGGAGGAGCAACAGCCGATGAGCGAGTAC 780
 QY 813 CCATTAGGGGTGTGACAGGAGCGGTGAGTAAACAGCAGCTGAGGAGACGAGCGCGAA 872
 Db 781 CCATTAGGGGTGTGACAGGAGCGGTGAGTAAACAGCAGCTGAGGAGACGAGCGCGAA 840
 QY 873 GGGTCCGCGCCCTTCCGCAAGTTCTATAGAGTGTGAGAGGAGGAGCCCTTTAAACCA 932
 Db 841 GGGTCCGCGCCCTTCCGCAAGTTCTATAGAGTGTGAGAGGAGGAGCCCTTTAAACCA 900
 QY 933 TCCTCAGCAAGACAGCTTTCCCAAGAGACAGAGTCCCTTGAAGTCCGAGAGTGGAA 992
 Db 901 TCCTCAGCAAGACAGCTTTCCCAAGAGACAGAGTCCCTTGAAGTCCGAGAGTGGAA 960
 QY 993 AGGTGACAGGGGATGTATGAAATTGCTGCTTCTGAGGCTCTTCAACAGAGTCC 1052
 Db 961 AGGTGACAGGGGATGTATGAAATTGCTGCTTCTGAGGCTCTTCAACAGAGTCC 1020
 QY 1053 TGTGAGAACCAACTTTGAGAGCCCAAGTCAATGGGGTTTACCCGCTTCTCACTCAT 1112
 Db 1021 TGTGAGAACCAACTTTGAGAGCCCAAGTCAATGGGGTTTACCCGCTTCTCACTCAT 1080
 QY 1113 AGAACCTTTCCCAATAGAGAAACCCCAAGGTAACTGAAATTTCCCTTCATGAG 1172
 Db 1081 AGAACCTTTCCCAATAGAGAAACCCCAAGGTAACTGAAATTTCCCTTCATGAG 1140
 QY 1173 GTAGAGAGAGGGGTCTCTCCCAATATTTCTTCTGTGCTCTCTTTATCAC 1232
 Db 1141 GTAGAGAGAGGGGTCTCTCCCAATATTTCTTCTGTGCTCTCTTTATCAC 1200
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 Db 1201 TTTTAAAGATA 1211

RESULT 7
 US-09-992-598-510
 / Sequence 510, Application US/09992598
 / Patent No. US20020160384A1
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerlitsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT FILING DATE: US/09/992,598
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
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PRIOR APPLICATION NUMBER: 60/088030
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PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi J.			
APPLICANT: Baker, Kevin P.			
APPLICANT: Botstein, David			
APPLICANT: Desnoyers, Luc			
APPLICANT: Baton, Dan L.			
APPLICANT: Ferrara, Napoleone			
APPLICANT: Fong, Sherman			
APPLICANT: Gerber, Hanspeter			
APPLICANT: Gerlitsen, Mary E.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Grimaldi, J. Christopher			
APPLICANT: Gurney, Austin L.			
APPLICANT: Kijavlin, Ivar J.			
APPLICANT: Napier, Mary A.			
APPLICANT: Pan, James			
APPLICANT: Paoni, Nicholas F.			
APPLICANT: Roy, Margaret Ann			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Watanabe, Colin K.			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William I.			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
FILE OF INVENTION: Acids Encoding the Same			
FILE REFERENCE: P2730PIC66			
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Db	259	GCTGTGCGCTTGTGACAGGCGTCTGCAGCATGAGCGTCTTCAGAGCGTATCCCAATGCGCTCC	318			
QY	234	CCACTGCTGGGCTTCAGCTGGGGTGGGCTGATCCACCTGTACACAGCCAGACCCAGGAAAC	293			
Db	319	CCACTGCTGGGCTTCAGCTGGGGTGGGCTGATCCACCTGTACACAGCCAGACCCAGGAAAC	378			
QY	294	AGCTTACACCTGCGAGATTCACAAAGAAATGGCCATGTGATGGCGCACCCCATCAGACCATC	353			
Db	379	AGCTTACACCTGCGAGATTCACAAAGAAATGGCCATGTGATGGCGCACCCCATCAGACCATC	438			
QY	354	TACAGTGGCGTGAATGATCAATCAGAGATGCTGGCTTTGGTGGATTAAGAGGTGATG	413			
Db	439	TACAGTGGCGTGAATGATCAATCAGAGATGCTGGCTTTGGTGGATTAAGAGGTGATG	498			
QY	414	AGCAGAAGATACCTCTGATGATGATTTTCAGAGGCAACATTTTGGATCACATATTTGAC	473			
Db	499	AGCAGAAGATACCTCTGATGATGATTTTCAGAGGCAACATTTTGGATCACATATTTGAC	558			
QY	474	CCGAGAACTGACAGTTTCCAAATCACAACGCTGGAAAACGGGTACGACGTCTACACTCT	533			
Db	559	CCGAGAACTGACAGTTTCCAAATCACAACGCTGGAAAACGGGTACGACGTCTACACTCT	618			
QY	534	CCTGATGATCACTTCGAGTCAATCTGGGCGGGCGAAGAGAGCTTCCGCAAGGATG	593			
Db	619	CCTGATGATCACTTCGAGTCAATCTGGGCGGGCGAAGAGAGCTTCCGCAAGGATG	678			
QY	594	AACCCACCCCGGTACTCCAGTTCTGTCCCGAGGAAACGAGATCCCTCATATTCATTC	653			
Db	679	AACCCACCCCGGTACTCCAGTTCTGTCCCGAGGAAACGAGATCCCTCATATTCATTC	738			
QY	654	AAACACCCCATACACGCGCGGACACCCCGAGGCGCGAGACATCTGGAGCGGAGACCC	713			
Db	739	AAACACCCCATACACGCGCGGACACCCCGAGGCGCGAGACATCTGGAGCGGAGACCC	798			

QY 714 CTGACGTCTGTAAGCCCGGCGGCGGATGACCCCGGCGGCTCTCTTCAAGAG 773
DB 799 CTGAAGCTGTGTAAGCCCGGCGGCGGATGACCCCGGCGGCTCTCTTCAAGAG 858
QY 774 CTCCGAGCCCGGAGCAACAGCCCGATGAGCCATTAAGGAGTGTAGGGGC 833
DB 859 CTCCGAGCCCGGAGCAACAGCCCGATGAGCCATTAAGGAGTGTAGGGGC 918
QY 834 GGTGAGTGAACAGCAGCGCTGGGGGAAAGGCGGCGGAGGCTCCGCTTCCCAAG 893
DB 919 GGTGAGTGAACAGCAGCGCTGGGGGAAAGGCGGCGGAGGCTCCGCTTCCCAAG 978
QY 894 TTCACTGAGGTGCTGG 911
DB 979 TTCACTGAGGTGCTGG 996

RESULT 11
US-09-989-730-510
Sequence 510, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 49.5%; Score 798; DB 9; Length 996;
 Best Local Similarity 100.0%; Pred. No. 2,3e-216;
 Matches 798; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 AATCTGACACCAACCACTAGAGCAGGACAGATGTTGGGGGCCCTCAGGCTCTGG 173
 DB 199 AATCTGACACCAACCACTAGAGCAGGACAGATGTTGGGGGCCCTCAGGCTCTGG 258
 QY 174 GTCTGTCCTTGTGACAGCCTGAGCATAGGCTCTCAGAGCTTATCCCATGCTCC 233
 DB 259 GTCTGTCCTTGTGACAGCCTGAGCATAGGCTCTCAGAGCTTATCCCATGCTCC 318
 QY 234 CCACTGCTGGCTCAAGCTGGGGTGGCTGATCACCCTGTACACAGCAGCAGGAAC 293
 DB 319 CCACTGCTGGCTCAAGCTGGGGTGGCTGATCACCCTGTACACAGCAGCAGGAAC 378
 QY 294 AGCTACCACTGACATCCACAGAAATGGCCATGTGATGGCCGACCCATCAGACCATC 353
 DB 379 AGCTACCACTGACATCCACAGAAATGGCCATGTGATGGCCGACCCATCAGACCATC 438
 QY 354 TACAGTCCCTGATGATCAGATGAGATGCTGGCTTGTGTGATTAAGTGTATG 413
 DB 439 TACAGTCCCTGATGATCAGATGAGATGCTGGCTTGTGTGATTAAGTGTATG 498
 QY 414 AGCAGAAATACCTCTGATGATTTCAAGAGCAATTTTGGATCACAATAATTGAC 473
 DB 499 AGCAGAAATACCTCTGATGATTTCAAGAGCAATTTTGGATCACAATAATTGAC 558
 QY 474 CCGAGAACTGACGGTTCCACACACAGCCTGGAACCGGGTACGACGTCTACACTCT 533
 DB 559 CCGAGAACTGACGGTTCCACACACAGCCTGGAACCGGGTACGACGTCTACACTCT 618
 QY 534 CTTCAATATCACTTCTGTGATCTGGGCGGAGGAGACCTTCTGCAAGGATG 593
 DB 619 CTTCAATATCACTTCTGTGATCTGGGCGGAGGAGACCTTCTGCAAGGATG 678
 QY 594 AACCCACCCCGTACTCCAGTCTGTCCTGGAGGAAGAGATCCCTTAATTCCTTC 653
 DB 679 AACCCACCCCGTACTCCAGTCTGTCCTGGAGGAAGAGATCCCTTAATTCCTTC 728
 QY 654 AACCCACCCATACCAAGGCGGACACCCCGAGGCGGAGACGATCGAGCGGACCC 713
 DB 739 AACCCACCCATACCAAGGCGGACACCCCGAGGCGGAGACGATCGAGCGGACCC 798
 QY 714 CTGAACGTGCTGAAGCCCGGGGCGGATGACCCCGGCTCTCTGTTCAAGAG 773
 DB 799 CTGAACGTGCTGAAGCCCGGGGCGGATGACCCCGGCTCTCTGTTCAAGAG 858
 QY 774 CTCCCGAGGCGGAGACACACAGCCGATGGCAGTGAATTAAGGGTGTCAAGGCG 833
 DB 859 CTCCCGAGGCGGAGACACACAGCCGATGGCAGTGAATTAAGGGTGTCAAGGCG 918
 QY 834 GGTGAGTGAACGACGCTGGGGGGAAGGGGCGGAGGCTGCGCCCTTGGCAAG 893
 DB 919 GGTGAGTGAACGACGCTGGGGGGAAGGGGCGGAGGCTGCGCCCTTGGCAAG 978
 QY 894 TTCATCTAGGGTGTGCTGG 911
 DB 979 TTCATCTAGGGTGTGCTGG 996

RESULT 12
 US-09-990-436-510
 ; Sequence 510, Application US/09990436
 ; Publication No. US20020198148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Ferrara, Napoleone

APPLICANT: Pong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuman, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088217
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PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445

Query Match	Similarity	49.5%	Score 798	DB 9	Length 996
Best Local	Similarity	100.0%	Pred. No. 2.3e-216		
Matches	798	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	114	AATCTCAGCAGCCAGCCACTCAGAGCAGGCGACGATTTGGGGGCCCGCTCAGAGCTCTGG	173		
Db	199	AATCTCAGCAGCCAGCCACTCAGAGCAGGCGACGATTTGGGGGCCCGCTCAGAGCTCTGG	258		
QY	174	GTCGTGCTTGTGTGAGCGCTCTGCAGCATAGCGTCTCAGAGCCTTATCCATGCTTCC	233		
Db	259	GTCGTGCTTGTGTGAGCGCTCTGCAGCATAGAGGTCCTCAGAGCCTTATCCATGCTTCC	318		
QY	234	CCACGCTGTGGGCTCCAGCTTGGGGGTGGCTCTGATTCACCTGTATCACAAGCCACAAGCAGGAAC	293		
Db	319	CCACGCTGTGGGCTCCAGCTTGGGGGTGGCTCTGATTCACCTGTATCACAAGCCACAAGCAGGAAC	378		
QY	294	AGCTTACCACTGTCAGATCCACAAGATGAGCATGTGTGATGAGCGGCAACCCCATCAGACATTC	353		
Db	379	AGCTTACCACTGTCAGATCCACAAGATGAGCATGTGTGATGAGCGGCAACCCCATCAGACATTC	438		
QY	354	TACAGTGCCTTGATGATTCAGATCAAGAGATGCTGGCTTTGTGTGATTTACAGGTGTGATG	413		
Db	439	TACAGTGCCTTGATGATTCAGATCAAGAGATGCTGGCTTTGTGTGATTTACAGGTGTGATG	498		
QY	414	AGCAGAGATACCTCTGCATGATTTACAAGGCAACATTTTGGATTCACATATTTTCAGC	473		
Db	499	AGCAGAGATACCTCTGCATGATTTACAAGGCAACATTTTGGATTCACATATTTTCAGC	558		

RESULT 13
US-09-991-181-510
Sequence 510, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyere, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER:	60/089105
PRIOR FILING DATE:	1998-06-12
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PRIOR FILING DATE:	1998-06-16
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PRIOR FILING DATE:	1998-06-16

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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-22

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PRIOR FILING DATE: 1998-07-09

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Query Match Similarity      49.5%; Score 798; DB 9; Length 996;
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Job time : 268 secs

GenCore version 5.1.4.D5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 21:20:14 ; Search time 72 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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C 43	42	2.6	540	3	US-08-643-704A-45	Sequence 45, App1
C 44	42	2.6	11517	1	US-07-920-281C-1	Sequence 1, App1
C 45	42	2.6	11517	4	US-08-466-277-1	Sequence 1, App1

ALIGNMENTS

RESULT 1
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Sequence 2, Application US/08187780
Patent No. 5459250
GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALANICO
TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 360 Kb storage
COMPUTER: IBM or IBM-compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,780
FILING DATE: January 25, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5986/13586-US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION:

HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: This sequence can be
 OTHER INFORMATION: found on page 5, lines 3-13, in the
 OTHER INFORMATION: PUBLICATION INFORMATION: as filed.
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO: 1-423
 US-08-187-780-2

Query Match 3.3%; Score 52.6; DB 1; Length 423;
 Best Local Similarity 52.4%; Pred. No. 0.00016;
 Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

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 QY 349 CCATCTACAGTGCCTGATGATGATGATGATGATGATGATGATGATGATG 408
 DB 134 CCGCGCAGAGCTCTGAGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 193
 QY 409 TGATGACGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 468
 DB 194 TGGCAGCGGCTTCTGATGATGATGATGATGATGATGATGATGATGATG 253
 QY 469 TCGACCGGAGAACTGAGGATTCACACGAGCGCTGAGAAAGGGTACGCTTACC 528
 DB 254 TCACCG---GATGATGATGATGATGATGATGATGATGATGATGATGATG 310
 QY 529 ACTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 555
 DB 311 AGTCTTACAGTACCGCGGCGATGTTCA 337

RESULT 2
 US-08-187-780-5
 Sequence 5, Application US/08187780
 Patent No. 5459250
 GENERAL INFORMATION:
 APPLICANT: CLAUDIO BASILICO
 APPLICANT: DANIELA TALARICO
 TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Darryl & Darryl P.C.
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch,
 MEDIUM TYPE: 360 KB storage
 COMPUTER: IBM or IBM-compatible
 OPERATING SYSTEM: PC/MS-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/187,780
 FILING DATE: January 25, 1994

CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/901,705
 FILING DATE: June 22, 1992
 APPLICATION NUMBER: 07/806,771
 FILING DATE: December 6, 1991
 APPLICATION NUMBER: 07/177,506
 FILING DATE: April 4, 1988
 APPLICATION NUMBER: 07/062,925
 FILING DATE: June 16, 1987
 ATTORNEY/AGENT INFORMATION:
 NAME: Howard M. Frankfort
 REGISTRATION NUMBER: 32,613
 REFERENCE/DOCKET NUMBER: 5986/13586-US3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 527-7700
 TELEFAX: (212) 753-6237
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 423
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 DESCRIPTION:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: This sequence
 OTHER INFORMATION: corresponds to K-FGF-140 and can be
 OTHER INFORMATION: found on page 11, lines 39-47 and page
 OTHER INFORMATION: 12, lines 1-31, in the application, as
 OTHER INFORMATION: filed.
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO: 1-423
 US-08-187-780-5

Query Match 3.3%; Score 52.6; DB 1; Length 423;
 Best Local Similarity 52.4%; Pred. No. 0.00016;
 Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

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 DB 74 GCATCGCTTCCACTCCAGGCGCTCCCGACGGCGCGCATGGCGCGCGAC 133
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 DB 134 CCGCGCAGAGCTCTGAGAGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 193
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 DB 254 TCACCG---GATGATGATGATGATGATGATGATGATGATGATGATGATG 310
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RESULT 3
 US-08-478-485-2
 Sequence 2, Application US/08478485
 Patent No. 5683071
 GENERAL INFORMATION:
 APPLICANT: CLAUDIO BASILICO
 APPLICANT: DANIELA TALARICO
 TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Darby & Darby P.C.
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Diskette, 3+ inch,
 MEDIUM TYPE: 1.44 MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC/MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/478,485
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/187,780
 FILING DATE: January 25, 1994
 APPLICATION NUMBER: 07/901,705
 FILING DATE: June 22, 1992
 APPLICATION NUMBER: 07/806,771
 FILING DATE: December 6, 1991
 APPLICATION NUMBER: 07/177,506
 FILING DATE: April 4, 1988
 APPLICATION NUMBER: 07/062,925
 FILING DATE: June 16, 1987
 ATTORNEY/AGENT INFORMATION:
 NAME: Joseph R. Robinson
 REGISTRATION NUMBER: 33,448
 REFERENCE/DOCKET NUMBER: 5986/13586-US6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 527-7700
 TELEFAX: (212) 753-6237
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 423
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 DESCRIPTION: Genomic DNA
 HYPOTHEICAL: No
 ANTI-SENSE: No
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: This sequence can be
 OTHER INFORMATION: found on page 5, lines 3-13, in the
 OTHER INFORMATION: application, as filed.
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO: 1-423

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US-08-478-485-2
Query Match          3.3%, Score 52.6; DB 2; Length 423;
Best Local Similarity 52.4%; Pred. No. 0.0016;
Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY      289   GGAACAGCTACCACTTGAGATCCACAAGATGGCGCATGTGATGCGCACCCCATCAGA    348
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
DB       74   GGATGGGCTTCACCTCCAGGGCGCTCCCCCGAGCGCGCATGGCGGCCGACGCGGACA    133
QY      349   CCATCTAACAGTGCCTCGTAGTTCAGATCAGAGAGATGCTGGCTTTGTGTGATTACAGGTG    408
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
DB      134   CCCGGACAGCCTGTGTGAGACTCTGCGCCCGAGACGGGCGGTGTGTGCAATCTTTCGCGG    193
QY      409   TGATAGACAGAAGATACTCTGCATGTGATTTCAAGAGGCACATTTTGTGATCACAATAATT    468
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
DB     194   TGGCAGACCGGTTCTTCTGGCGCATGAGACAGACAGGGGCAAGCTGTATGTCTGCGCTTCT    253
QY      469   TCGACCCCGAAGAACTGCAAGGTTCCACAACCAAGACGCTGGAAAAGGGGTAGCACTTAACC    528
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
DB     254   TCACC--GAAGAGAGCAACGTTCAAAGAGAGATTCTTCCCAACAATAACAACGCTACG    310
QY      529   ACTCTCTCAGTATCATCTTCTGTGCA    555
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| |
DB     311   AGTCTACAAGTACCCGCGCATGTTCA    337

RESULT 4
US-08-478-485-5
Sequence 5, Application US/08478485
Patent No. 5883071
GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette, 3+ inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,485
FILING DATE: Concurrently Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
FILING DATE: January 25, 1994
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Joseph R. Rodinson
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 5986/13586-US6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
```

LENGTH: 423
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Genomic DNA
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: This sequence
OTHER INFORMATION: corresponds to K-FGF-140 and can be
OTHER INFORMATION: found on page 11, lines 39-47 and page
OTHER INFORMATION: 12, lines 1-31, in the application, as
PUBLICATION INFORMATION: filed.
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 1-423
US-08-478-485-5

Query Match 3.3%; Score 52.6; DB 2; Length 423;
Best Local Similarity 52.4%; Pred. No. 0.00016;

Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAACGCTCCACCTGCAATCCAAAGATGCGCATGTGGAGCGCACCCCATCAGA 348
DB 74 GCATCGGCTTCACCTCCAGCGCTCCCGGCGCGCATGCGGCGCGGCGGACGA 133
QY 349 CCATCTACAGTGCCTGATGATCAGATCAGAGATGCGCTTGTGGTATACAGGTG 408
DB 134 CCGGCAACACCTGCTGAGCTCTCGCCGCGGAGCGGCGGTGTGAGCATCTTCGCG 193
QY 409 TGATGACAGAAATACCTCTGATGATTTCAAGAGCAATTTTGGATCACTATT 468
DB 194 TGCCAGCGCGTCTTCTGCGCCATGAGCAGCAAGGCAAGCTTATGCGTCCCTTCT 253
QY 469 TCACCCGAGAACTGAGGTTCCAAACAGACGCTGAAAAAGCGGTACGAGCTTACC 528
DB 254 TCACCC--GATGAGTGACGCTTCAAGAGATTTCTTCCCAACACTACACGCTACG 310
QY 529 ACTCTCCTAGTATCACTTCTGTGCA 555
DB 311 AGTCTTACAGTACCCCGGAGTTCA 337

RESULT 5

US-08-478-486F-2

Sequence 2, Application US/08478486F
Patent No. 6432702
GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette, 3+ inch,
MEDIUM TYPE: 1.44 MB storage

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478, 486F
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
FILING DATE: January 25, 1994
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5986/13586-US7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: Genomic DNA
HYPOTHETICAL: No
ANTI-SENSE: No
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: This sequence can be
OTHER INFORMATION: found on page 5, lines 3-13, in the
OTHER INFORMATION: application, as filed.
US-08-478-486F-2

Query Match 3.3%; Score 52.6; DB 4; Length 423;
Best Local Similarity 52.4%; Pred. No. 0.00016;
Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAACGCTCCACCTGCAATCCAAAGATGCGCATGTGGAGCGCACCCCATCAGA 348
DB 74 GCATCGGCTTCACCTCCAGCGCTCCCGGCGCGCATGCGGCGCGGCGGACGA 133
QY 349 CCATCTACAGTGCCTGATGATCAGATCAGAGATGCGCTTGTGGTATACAGGTG 408
DB 134 CCGGCAACACCTGCTGAGCTCTCGCCGCGGAGCGGCGGTGTGAGCATCTTCGCG 193
QY 409 TGATGACAGAAATACCTCTGATGATTTCAAGAGCAATTTTGGATCACTATT 468
DB 194 TGCCAGCGCGTCTTCTGCGCCATGAGCAGCAAGGCAAGCTTATGCGTCCCTTCT 253
QY 469 TCACCCGAGAACTGAGGTTCCAAACAGACGCTGAAAAAGCGGTACGAGCTTACC 528
DB 254 TCACCC--GATGAGTGACGCTTCAAGAGATTTCTTCCCAACACTACACGCTACG 310
QY 529 ACTCTCCTAGTATCACTTCTGTGCA 555
DB 311 AGTCTTACAGTACCCCGGAGTTCA 337

RESULT 6

US-08-478-486F-5

Sequence 5, Application US/08478486F
Patent No. 6432702

GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette, 3+ inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,486F
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
FILING DATE: January 25, 1994
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5986/13586-US7
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 423
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Genomic DNA
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: This sequence
OTHER INFORMATION: corresponds to K-FGF-140 and can be
OTHER INFORMATION: found on page 11, lines 39-47 and page
OTHER INFORMATION: 12, lines 1-31, in the application, as
OTHER INFORMATION: filed.
US-08-478-486F-5

Query Match 3.3%; Score 52.6; DB 4; Length 423;
Best Local Similarity 52.4%; Pred. No. 0.00016;
Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAAGAGCTACCACTGCAATCACAAGATGGCCATGTGGATGGGACCCCATAGA 348
DB 74 GCAATCGGCTTCACCTCCAGCGCTCCCGACGCGCCATCGCGGCGCCACGCGACA 133
QY 349 CCATCTACAGTGCCTGATGATCAGATCAGAGATGCTGGCTTTGTGATTAACAGTG 408
DB 134 CCGGACAGCCCTGCTGACTCTCGCCCTGAGCGGGGCGTGTAGCATCTTCGCGC 193
QY 409 TGATGAGCAAGATACCTGTGATGATTTTCAGAGCAACATTTTGTATCAACATATT 468

DB 194 TGCCAGCCGGTTCTGTGCGCATGAGCAGCAAGGCAAGCTATATGGCTCGCCCTTCT 253
QY 469 TCGACCCGGAAGACTGAGAGTTCCACACAGACGCTGGAAGACGGGTACGAGCTTACC 528
DB 254 TCACCC--GATGAGTGACCTTCAGAGAGATTTCTTCCCAACACTACAGCCCTAACG 310
QY 529 ACTGTCTCAGTATCACTTCTGTGCA 555
DB 311 AGTCTTCAAGTACCCCGCATGTTCA 337

RESULT 7
US-08-478-486F-10
Sequence 10, Application US/08478486F
Patent No. 6432702
GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette, 3+ inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,486F
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
FILING DATE: January 25, 1994
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5986/13586-US7
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-478-486F-10

Query Match 3.3%; Score 52.6; DB 4; Length 528;
Best Local Similarity 52.4%; Pred. No. 0.00018;
Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAAGAGCTACCACTGCAATCACAAGATGGCCATGTGGATGGGACCCCATAGA 348
DB 182 GCAATCGGCTTCACCTCCAGCGCTCCCGACGCGCCATCGCGGCGCCACGCGACA 241
QY 349 CCATCTACAGTGCCTGATGATCAGATCAGAGATGCTGGCTTTGTGATTAACAGTG 408

Db 242 CCGGGAAGCCTGCTGAGCTCTGCGCCGCGAGCGGGCGTGGAGCATTTGCGCG 301
 QY 409 TGATGAGCAGAGATACCTTCATGATTTGAGAGCAATTTTGGATCACTATT 468
 Db 302 TGGCAGCGGTTCTTCTGCGCATGAGAGAGGAGGAGCTCTATGCTGCGCTTCT 361
 QY 469 TCGACCGGAGAACTGCAAGTTCCAAACGAGCGTGAAGGAGTACGACTTACC 528
 Db 362 TCACC---GATGAGTGACAGTTCAAGAGATTTCTTCCCAACAACAGCGCTACG 418
 QY 529 ACTCTCCCTCATATACCTTCTGCTCA 555
 Db 419 AGTCTTACAAGTACCCGCGCATGTTCA 445

RESULT 8
 5430019-1
 ; Patent No. 5430019
 ; APPLICANT: ROGERS, DAVID T.; WOLFMAN, NEIL M.; SEEHRA, JASBIR S.
 ; TITLE OF INVENTION: HOMOGENEOUS K-PGF AND USE OF THE SAME
 ; NUMBER OF SEQUENCES: 2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/898,051
 ; FILING DATE: 12-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 438,278
 ; FILING DATE: 16-NOV-1989
 ; SEQ ID NO:1:
 ; LENGTH: 599
 5430019-1

Query Match 3.3%; Score 52.6; DB 6; Length 599;
 Best Local Similarity 52.4%; Pred. No. 0.00019;
 Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAACAGCTACCACTGATGATCCAAAGATGCGCATGATGCGCACCCCATCAGA 348
 Db 185 GCATCGGCTTCCACTCCAGCGCTCCCGGCGCATGCGGCGCGCGACGAGACA 244
 QY 349 CCATCTACAGTCCCTGATATGATGATGAGATGCTGCTTTGTTGATTAAGGTG 408
 Db 245 CCGGCGACGCTGCTGAGCTCTGCGCCGCGTGAAGCGGCGGTGATGATCTTGGCG 304
 QY 409 TGATGAGCAGAGATACCTTCATGATTTGAGAGCAATTTTGGATCACTATT 468
 Db 305 TGGCAGCGGTTCTTCTGCGCATGAGAGAGGAGGAGCTCTATGCTGCGCTTCT 364
 QY 469 TCGACCGGAGAACTGAGTTCCAAACGAGCGTGAAGGAGTACGACTTACC 528
 Db 365 TCACC---GATGAGTGACAGTTCAAGAGATTTCTTCCCAACAACAGCGCTACG 421
 QY 529 ACTCTCCCTCATATACCTTCTGCTCA 555
 Db 422 AGTCTTACAAGTACCCGCGCATGTTCA 448

RESULT 9
 US-08-478-486F-9
 ; Sequence 9, Application US/08478486F
 ; Patent No. 6432702
 ; GENERAL INFORMATION:
 ; APPLICANT: CLAUDIO BASILICO
 ; APPLICANT: DANIELA TALARICO
 ; TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby P.C.
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Diskette, 3+ inch,
 MEDIUM TYPE: 1.44 MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC/MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/478,486F
 FILING DATE: June 7, 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/187,780
 FILING DATE: January 25, 1994
 APPLICATION NUMBER: 07/901,705
 FILING DATE: June 22, 1992
 APPLICATION NUMBER: 07/806,771
 FILING DATE: December 6, 1991
 APPLICATION NUMBER: 07/177,506
 FILING DATE: April 4, 1988
 APPLICATION NUMBER: 07/062,925
 FILING DATE: June 16, 1987
 ATTORNEY/AGENT INFORMATION:
 NAME: Howard M. Frankfort
 REGISTRATION NUMBER: 32,613
 REFERENCE/DOCKET NUMBER: 5986/13586-US7
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 527-7700
 TELEFAX: (212) 753-6237
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-478-486F-9

Query Match 3.3%; Score 52.6; DB 4; Length 618;
 Best Local Similarity 52.4%; Pred. No. 0.00019;
 Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAACAGCTACCACTGATGATCCAAAGATGCGCATGATGCGCACCCCATCAGA 348
 Db 272 GCATCGGCTTCCACTCCAGCGCTCCCGGCGCATGCGGCGCGCGACGAGACA 331
 QY 349 CCATCTACAGTCCCTGATATGATGATGAGATGCTGCTTTGTTGATTAAGGTG 408
 Db 332 CCGGCGACGCTGCTGAGCTCTGCGCCGCGTGAAGCGGCGGTGATGATCTTGGCG 391
 QY 409 TGATGAGCAGAGATACCTTCATGATTTGAGAGCAATTTTGGATCACTATT 468
 Db 392 TGGCAGCGGTTCTTCTGCGCATGAGAGGAGGAGCTCTATGCTGCGCTTCT 451
 QY 469 TCGACCGGAGAACTGAGTTCCAAACGAGCGTGAAGGAGTACGACTTACC 528
 Db 452 TCACC---GATGAGTGACAGTTCAAGAGATTTCTTCCCAACAACAGCGCTACG 508
 QY 529 ACTCTCCCTCATATACCTTCTGCTCA 555
 Db 509 AGTCTTACAAGTACCCGCGCATGTTCA 535

RESULT 10
 US-08-478-486F-11
 ; Sequence 11, Application US/08478486F
 ; Patent No. 6432702
 ; GENERAL INFORMATION:
 ; APPLICANT: CLAUDIO BASILICO
 ; APPLICANT: DANIELA TALARICO
 ; TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby P.C.
 ; STREET: 805 Third Avenue

```

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette, 3+ inch,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,486F
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
FILING DATE: January 25, 1994
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5986/13586-US7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1142 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-478-486F-11

Query Match
Best Local Similarity 52.4%; Score 52.6; DB 4; Length 1142;
Pred. No. 0.00027;
Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAAGCTACACCTGCAATCCACAGAAATGGCCATGTGGATGGGCAACCCCATAGA 348
DB 514 GCATGGCTTCACCTCCAGCGCTCCCGACGCGCGCATCGGCGCGCGACGAGCA 573
QY 349 CCATCTACAGTCCCTGATGATCAGATCAGAGATGCTGCTTGTGGTATTAAGGTG 408
DB 574 CCGGACAGACCTGCTGAGCTTCGCGCGGAGCGGGGCTGTAGACATCTTCCGCG 633
QY 409 TGATGACAGAAATACCTTGATGATTTCAAGGCAACATTTTGGATCACTATT 468
DB 634 TGGCAGCGCGTCTTGTGGCCATGAGCAGCAAGGCAAGCTCTATGCTCGCTTCT 693
QY 469 TCGACCCGGAAGTGCAGGTTCCAAACACAGACGCTGGAAAACGGGTACGAGCTTACC 528
DB 694 TCACCC--GATGAGTGACAGTTCAAGAGATTTCTCTCCCAACAACACTAAGACCTAAG 750
QY 529 ACTCTCTCATGATCACTTCTGTGCA 555
DB 751 AGTCTTACAAGTACCCGCGCATGTTC 777

RESULT 11
PCT-US93-06251-11
Sequence 11, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

```

```

NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digililo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-11

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Query Match
Best Local Similarity 52.4%; Score 52.6; DB 5; Length 1219;
Pred. No. 0.00028;
Matches 140; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 289 GGAAGCTACACCTGCAATCCACAGAAATGGCCATGTGGATGGGCAACCCCATAGA 348
DB 591 GCATGGCTTCACCTCCAGCGCTCCCGACGCGCGCATCGGCGCGCGACGAGCA 650
QY 349 CCATCTACAGTCCCTGATGATCAGATCAGAGATGCTGCTTGTGGTATTAAGGTG 408
DB 651 CCGGACAGACCTGCTGAGCTTCGCGCGGAGCGGGGCTGTAGACATCTTCCGCG 710
QY 409 TGATGACAGAAATACCTTGATGATTTCAAGGCAACATTTTGGATCACTATT 468
DB 711 TGGCAGCGCGTCTTGTGGCCATGAGCAGCAAGGCAAGCTCTATGCTCGCTTCT 770
QY 469 TCGACCCGGAAGTGCAGGTTCCAAACACAGACGCTGGAAAACGGGTACGAGCTTACC 528
DB 771 TCACCC--GATGAGTGACAGTTCAAGAGATTTCTCTCCCAACAACACTAAGACCTAAG 827
QY 529 ACTCTCTCATGATCACTTCTGTGCA 555
DB 828 AGTCTTACAAGTACCCGCGCATGTTC 854

RESULT 12
US-07-915-934-1
Sequence 1, Application US/07915934
Patent No. 5360893
GENERAL INFORMATION:
APPLICANT: OWENS, GREGORY P.
APPLICANT: COHEN, J. J.
APPLICANT: HAHN, WILLIAM E.
TITLE OF INVENTION: DNA SEQUENCES ENCODING PROTEINS USED TO
; TITLE OF INVENTION: ELICIT AND DETECT PROGRAMMED CELL DEATH
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302

```

CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,934
FILING DATE: 19920720
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 92-0224.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 972 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..864
US-07-915-934-1

Query Match 2.8%; Score 45.8; DB 1; Length 972;
Best Local Similarity 67.0%; Pred. No. 0.015;
Matches 65; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1178 GAGAGGGGCTCTCCCAACATATTTCTTCTGTCCTCTCTTATCACTTTA 1237
DB 863 GAAGGTGTAAATTTCTTAAATTAATGTTCTTATGCTCTCACTCAAAAAA 922
QY 1238 AGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
DB 923 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 959

RESULT 13
US-08-325-743-1
Sequence 1, Application US/08325743
Patent No. 5527682
GENERAL INFORMATION:
APPLICANT: OWENS, GREGORY P.
APPLICANT: COHEN, J. J.
APPLICANT: HAHN, WILLIAM E.
TITLE OF INVENTION: DNA SEQUENCES ENCODING PROTEINS USED TO
NUMBER OF INVENTIONS: ELICIT AND DETECT PROGRAMMED CELL DEATH
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.
STREET: 11545 W. BERNARDO COURT, STE. 302
CITY: SAN DIEGO
STATE: CA
COUNTRY: USA
ZIP: 92127
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,743
FILING DATE: 19-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/915,934
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 92-0224.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 451-1120
TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 972 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..864
US-08-325-743-1

Query Match 2.8%; Score 45.8; DB 1; Length 972;
Best Local Similarity 67.0%; Pred. No. 0.015;
Matches 65; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1178 GAGAGGGGCTCTCCCAACATATTTCTTCTGTCCTCTCTTATCACTTTA 1237
DB 863 GAAGGTGTAAATTTCTTAAATTAATGTTCTTATGCTCTCACTCAAAAAA 922
QY 1238 AGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
DB 923 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 959

RESULT 14
US-09-240-952-1
Sequence 1, Application US/09240952
Patent No. 633523
GENERAL INFORMATION:
APPLICANT: Kljavin, Ivar
APPLICANT: La Fleur, Monique
TITLE OF INVENTION: Method of Preventing the Death of Retinal
NUMBER OF INVENTIONS: Neurons and Treating Ocular Diseases
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,952
FILING DATE: 29-Jan-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/041,383
FILING DATE: 12-Mar-98
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1088P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs

TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-240-952-1

Query Match 2.8%; Score 45.2; DB 4; Length 800;
Best Local Similarity 50.0%; Pred. No. 0.02;
Matches 141; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

QY 251 CTGGGGTGGCTGATCCAGCTGTACACAGCCAGCCAGGAAGCTACCTGCAAGAT 310
DB 214 CTGGGGGCGCGGACCGGACCGCTCTACTGAGAGTGGGATCGGTTCCATCTGCAGAT 273
QY 311 CCACAGAAATGGCCATGTGATGGCGCACCCATCAGACCACTTACAGTGCCTGATGAT 370
DB 274 CTACCCGAGATGGCAAGTCAATGATCCCAAGAGCCAAATATGTTAAGTGTGGAAAT 333
QY 371 CAGATCAGAGATGCTGGCTTTGTGTGATTAACAGGTGTGATGAGCAGAAAGATACCTG 430
DB 334 ATTTGCTGTCTCAGGGAGTTGTAGAAATACGAGAGTTTTCAGCAACAATTTTTCAGC 393
QY 431 CATGATTTTCAAGGCAACATTTTGGATCACTATTTGACCCGGAAGTGCAGGTT 490
DB 394 GATGTCAAAAAAGAAATCTCCATGCAAGTCCCAAGTTCA--CAGATGACTGCAAGTT 450
QY 491 CCAACACACAGACGCTGAAAAACGGGTACGACGTCTACCACTC 532
DB 451 CAGGAGCGCTTTTCAAGAAATAGCTAATAATACCTATGCCCTC 492

RESULT 15
US-09-484-970B-167
Sequence 167, Application US/09484970B
Patent No. 6426186

GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
SEQ ID NO 167
LENGTH: 1234
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 333034.1
US-09-484-970B-167

Query Match 2.8%; Score 45.2; DB 4; Length 1234;
Best Local Similarity 50.0%; Pred. No. 0.025;
Matches 141; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

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DB 499 CTGGGGGCGCGGACCGGACCGCTCTACTGAGAGTGGGATCGGTTCCATCTGCAGAT 558
QY 311 CCACAGAAATGGCCATGTGATGGCGCACCCATCAGACCACTTACAGTGCCTGATGAT 370
DB 559 CTACCCGAGATGGCAAGTCAATGATCCCAAGAGCCAAATATGTTAAGTGTGGAAAT 618
QY 371 CAGATCAGAGATGCTGGCTTTGTGTGATTAACAGGTGTGATGAGCAGAAAGATACCTG 430
DB 619 ATTTGCTGTCTCAGGGAGTTGTAGAAATACGAGAGTTTTCAGCAACAATTTTTCAGC 678
QY 431 CATGATTTTCAAGGCAACATTTTGGATCACTATTTGACCCGGAAGTGCAGGTT 490
DB 679 GATGTCAAAAAAGAAATCTCCATGCAAGTCCCAAGTTCA--CAGATGACTGCAAGTT 735

QY 491 CCAACACACAGACGCTGAAAAACGGGTACGACGTCTACCACTC 532
DB 736 CAGGAGCGCTTTTCAAGAAATAGCTAATAATACCTATGCCCTC 777
Search completed: May 29, 2003, 00:07:03
Job time : 82 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 28, 2003, 21:20:14 ; Search time 4519 Seconds

(without alignments)
10381.439 Million cells updates/sec

Title: US-09-901-938-1

Perfect score: 1612
Sequence: 1 cggcaaaaaggaggggaatcc.....tgagacactctcgtctcgct 1612

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
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12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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24: em_ph:*
25: em_pl:*
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28: em_un:*
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30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hgo_hum:*
40: em_hgo_mus:*
41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1612	100.0	1612	9 AF263537	AF263537 Homo sapi
2	1598	99.1	3004	9 AB047858	AB047858 Homo sapi
3	1211	75.1	1211	6 AX191707	AX191707 Sequence
4	1151	71.4	170200	9 AC008012	AC008012 Homo sapi
5	798	49.5	996	6 AX403623	AX403623 Sequence
6	756	46.9	996	6 AX464132	AX464132 Sequence
7	756	46.9	756	6 AX249749	AX249749 Sequence
8	756	46.9	756	6 AX250102	AX250102 Sequence
9	756	46.9	756	6 AX481467	AX481467 Sequence
10	756	46.9	756	6 AB037973	AB037973 Homo sapi
11	753	46.7	753	6 AX235431	AX235431 Sequence
12	528	32.8	753	6 AX191709	AX191709 Sequence
13	457.4	28.4	1559	10 AF263536	AF263536 Mus muscu
14	448.8	27.8	756	10 AB078777	AB078777 Rattus no
15	428	26.6	756	6 AX249747	AX249747 Sequence
16	428	26.6	756	6 AX250100	AX250100 Sequence
17	428	26.6	756	10 AB037889	AB037889 Mus muscu
18	234.2	14.5	76884	2 AC103292	AC103292 Rattus no
19	234.2	14.5	204909	2 AC1030862	AC1030862 Rattus no
20	230.8	14.3	178533	2 AC015538	AC015538 Mus muscu
21	205.8	12.8	204809	2 AC130862	AC130862 Rattus no
22	76.2	4.7	290471	2 AC125991	AC125991 Rattus no
23	73.2	4.5	624	6 AX191715	AX191715 Sequence
24	72.8	4.5	514	6 AX097639	AX097639 Sequence
25	72.6	4.5	651	6 AX481448	AX481448 Sequence
26	72.6	4.5	651	9 AB018122	AB018122 Homo sapi
27	72.6	4.5	1869	9 BC017664	BC017664 Homo sapi
28	72.6	4.5	2137	6 AX076894	AX076894 Sequence
29	72.6	4.5	2137	6 AX092981	AX092981 Sequence
30	72.6	4.5	2137	6 AX403730	AX403730 Sequence
31	72.6	4.5	2137	6 AX454492	AX454492 Sequence
32	72.6	4.5	2137	6 AX490970	AX490970 Sequence
33	72.6	4.5	2157	9 AF110400	AF110400 Homo sapi
34	72.4	4.5	630	6 AX156436	AX156436 Sequence
35	72.4	4.5	630	6 AX481451	AX481451 Sequence
36	72.4	4.5	630	9 AB021975	AB021975 Homo sapi
37	72.4	4.5	643	6 AX149492	AX149492 Sequence
38	72.4	4.5	784	6 AX156434	AX156434 Sequence
39	72.4	4.5	882	6 AX191713	AX191713 Sequence
40	72.4	4.5	939	6 AX358824	AX358824 Sequence
41	72.4	4.5	939	6 AX362317	AX362317 Sequence
42	72.4	4.5	1117	6 AX351022	AX351022 Sequence
43	72.4	4.5	1190	6 AX275042	AX275042 Sequence
44	72.4	4.5	1362	9 BC018404	BC018404 Homo sapi
45	68.4	4.2	633	10 AB025718	AB025718 Mus muscu

ALIGNMENTS

RESULT 1	AF263537	1612 bp	mRNA	linear	PII 14-DEC-2000
LOCUS	AF263537				
DEFINITION	Homo sapiens RGF23 (RGF23) mRNA, complete cds.				
ACCESSION	AF263537				
VERSION	AF263537.1	GI:9964291			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens.				
	Homo sapiens.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 1612)				
AUTHORS	White,K.B., Evans,W.E., O'Riordan,J.L.H., Speer,M.C., Econs,M.J.,				
	Lorenz-Deleureux,B., Grabowski,M., Meitinger,T. and Strom,T.M.				
TITLE	Autosomal dominant hypophosphataemic rickets is associated with				

QY 1455 CCTTGTCTTCTCTTGAGACATCTCTGGGAGAGAGCTGTCAAAAGACTGGTGAGGCTGG 1514
 DB 1441 CTTTCTTCTTCTCTTGAGACATCTCTGGGAGAGAGCTGTCAAAAGACTGGTGAGGCTGG 1500
 QY 1515 TGAAGACTTGACAGCTAGATGATGCTTCTGATAATGAGGCGAGATCTAATATGAAAA 1574
 DB 1501 TGAAGACTTGACAGCTAGATGATGCTTCTGATAATGAGGCGAGATCTAATATGAAAA 1560
 QY 1575 CTCAGCTCTCTGACAGGAGGAGACCTTCTGTCTGCT 1612
 DB 1561 CTCAGCTCTCTGACAGGAGGAGACCTTCTGTCTGCT 1598
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 AX191707 AX191707 1211 bp DNA linear PAT 15-AUG-2001
 LOCUS Sequence 1 from Patent WO0149740.
 ACCESSION AX191707
 VERSION AX191707.1 GI:15209882
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 1 (bases 1 to 1211)
 AUTHORS Conklin,D.C.
 TITLE Novel fzf homolog zfgf12
 JOURNAL Patent: WO 0149740-A 1 12-Jul-2001;
 ZymoGenetics, Inc. (US)
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 /db_xref="taxon:9606"
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 /note="unnamed protein product"
 /codon_start=1
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 /db_xref="GI:15209883"
 /translation="MLGARLRMLVCAICGVCMSVIRAPNAPSPLIGSWSGLIHLYT
 ATARNSYHLQIHKNQHVDAEPHOTIYSALMISEDAQFVITGVMSRRLICMDPFGNI
 FGSHPFDENCRFPOHOLENGYDVHSPQYHFLVLSIGRAKRAFLPQMNPYPSPQLSR
 RNEIPLIHNTPIPRHTRSADDESDERDLNLTKPRAKMTAPAPASCSQGLPFAEDNSP
 MASDPLGVVRGVRNTHAGTGTEGRCRPAKFI"
 BASE COUNT 273 a 380 c 321 g 237 t
 ORIGIN
 Query Match 75.1%; Score 1211; DB 6; Length 1211;
 Best Local Similarity 100.0%; Pred. No. 2.3e-281;
 Matches 1211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 393 GTGGATTAACAGGTGTGATGAGCAGAAAGATACCTCTGCATGATTTTCAAGAGCAAT 452
 DB 361 GTGGATTAACAGGTGTGATGAGCAGAAAGATACCTCTGCATGATTTTCAAGAGCAAT 420
 QY 453 TTTGATCAACTATTTCAGACCCGGAGAACTGCAAGTTCCAAACAGCAGAGCGTGAAG 512
 DB 421 TTTGATCAACTATTTCAGACCCGGAGAACTGCAAGTTCCAAACAGCAGAGCGTGAAG 480
 QY 513 GGGTACAGAGTCTACACACTCTCTCAGTATCACTTCTGTGATGAGTGGGCGGGGAG 572
 DB 481 GGGTACAGAGTCTACACACTCTCTCAGTATCACTTCTGTGATGAGTGGGCGGGGAG 540
 QY 573 AGAGCTTCTGACAGAGCAGTAAACCCACCCCGTACTCCAGTCTCTGTCGGAGAGAAC 632
 DB 541 AGAGCTTCTGACAGAGCAGTAAACCCACCCCGTACTCCAGTCTCTGTCGGAGAGAAC 600
 QY 633 GAGATCCCCCTAATTCACTTCAACACCCCATACAGAGCGGACACCCGAGCGCGAG 692
 DB 601 GAGATCCCCCTAATTCACTTCAACACCCCATACAGAGCGGACACCCGAGCGCGAG 660
 QY 693 GACGACTGAGAGGGGACCCCTGAAAGTCTGAGAGCCCGGCGCGATGACCCCGGCC 752
 DB 661 GACGACTGAGAGGGGACCCCTGAAAGTCTGAGAGCCCGGCGCGATGACCCCGGCC 720
 QY 753 CCGGCTCTCTGTTCAAGAGAGTCCCGAGCGCGGAGAGACACAGCCCATGCGCATGAC 812
 DB 721 CCGGCTCTCTGTTCAAGAGAGTCCCGAGCGCGGAGAGACACAGCCCATGCGCATGAC 780
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 DB 781 CCATTAGGGGTGATGAGGGGCGGTGAGTGAACAAGCAGCTGGGGGAGACGGGCGCGAA 840
 QY 873 GGCTGCGGCCCTTTCGCAAGTTCATCTAGAGTGGCTGAGAGGGACCCCTTTTAAACCA 932
 DB 841 GGCTGCGGCCCTTTCGCAAGTTCATCTAGAGTGGCTGAGAGGGACCCCTTTTAAACCA 900
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 QY 993 AGGTGACAGGGGACATGATGAATTTGCTGCTCTGGGGTCCCTTCCACAGAGGCTC 1052
 DB 961 AGGTGACAGGGGACATGATGAATTTGCTGCTCTGGGGTCCCTTCCACAGAGGCTC 1020
 QY 1053 TGTGAACAACACTTTGAGGCCCAAGTATGAGGTTTACAGCCCTTCTCACTCCATAT 1112
 DB 1021 TGTGAACAACACTTTGAGGCCCAAGTATGAGGTTTACAGCCCTTCTCACTCCATAT 1080
 QY 1113 AGAACACTTTTCCAAATGAGAAACCCCAACAGATAACTGAAATTTCCCTTCAAGAG 1172
 DB 1081 AGAACACTTTTCCAAATGAGAAACCCCAACAGATAACTGAAATTTCCCTTCAAGAG 1140
 QY 1173 GTAGAGAGAGGGTCTCTCCCAATATTTCTTCTTGTGCTCTCTTATATC 1232
 DB 1141 GTAGAGAGAGGGTCTCTCCCAATATTTCTTCTTGTGCTCTCTTATATC 1200
 QY 1233 TTTTAAGCATA 1243
 DB 1201 TTTTAAGCATA 1211
 RESULT 4
 AC008012 AC008012 170200 bp DNA linear PRI 15-MAR-2002
 LOCUS Homo sapiens 12p13 BAC RPc111-388F6 (Roswell Park Cancer Institute
 DEFINITION Human BAC library) complete sequence.
 ACCESSION AC008012
 VERSION AC008012.8 GI:5762548
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 170200)

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Muzny, D., Aronson, A.D., Bouck, J., Bunac, C., Chen, Z., Ding, Y.,
Dugan, S., Durbin, J., Forcum, J., Garcia, C., Gorrell, J.H.,
Gorrell, L.L., Hernandez, J., Issa, A., Jackson, L., Kneitz, S.,
Kondajewski, N., Lau, S., Leal, B., Lee, E., Lichtarge, O., Liu, W.,
Logan, O., Lu, J., Marondel, I., Martinez, C., Merscher, S., Miller, A.,
Montgomery, K., Oswal, G., Pampell, L.R., Parish, B.J., Perez, L.,
Rashid, N.D., River, C., Scherer, S.E., Shen, H., Shim, C., Simon, M.,
Vo, Q., Williamson, A., Worley, K.C., Xiang, A.W., Yang, R., Yu, W.,
Zhou, X., Zuchner, R., Nelson, D. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 170200)
Worley, K.C.
Direct Submission
Submitted (10-JUL-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 170200)
Worley, K.C.
Direct Submission
Submitted (24-AUG-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 170200)
Worley, K.C.
Direct Submission
Submitted (09-OCT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 170200)
Worley, K.C.
Direct Submission
Submitted (28-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 170200)
Worley, K.C.
Direct Submission
Submitted (15-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 24, 1999 this sequence version replaced gi:5708398.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----
Contig length: 170200
Phrap values in estimate: 169098
Average error rate (BCM-Phrap estimate): 0.000234169
Fraction of Phrap values less than 40 : 0.0503199
Number of consensus changing edits: 21
Number of N's in consensus : 0

----- Consensus changing edits -----
Position Original+Context Edited+Context
14775 attccaaaaa(n)ttatattacg attccaaaaa(n)ttatattacg
33904 ggaacacaca(n)aaaaagacc ggaacacaca(n)aaaaagacc
50944 tacttaacat(n)tcctctctt tacttaacat(n)tcctctctt
51576 ctatagat(n)tgtagtgtag ctatagat(n)tgtagtgtag
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 VERSION AX403623.1 GI:21437088
 KEYWORDS
 SOURCE
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D.,
 Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,
 Grimaldi, C.T., Gurney, A.L., Kijavrin, I., Napier, M.A., Pan, J.,


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LOCUS AX249749
DEFINITION Sequence 3 from Patent WO0166596.
ACCESSION AX249749
VERSION AX249749.1 GI:15864369
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS Itch,N. and Kavanagh,M.W.
TITLE Human fgf-23 gene and gene expression products
JOURNAL Patent: WO 0166596-A 3 13-SEP-2001;
CHIRON CORPORATION (US) ; Kyoto University (JP)
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Best Local Similarity 100.0%; Pred. No. 1.4e-171;
Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 3 from Patent WO0166595.
ACCESSION AX250102
VERSION AX250102.1 GI:15864511
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 756)
AUTHORS Itch,N. and Kavanagh,M.W.
TITLE Human fgf-23 gene and gene expression products
JOURNAL Patent: WO 0166595-A 3 13-SEP-2001;
CHIRON CORPORATION (US) ; Kyoto University (JP)
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Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 ATGTTGGGGGCGCCCTCAGGCTCTGGGCTGTGCTGTGCGAGCGTCTGACAGATGAGC 206
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 ORGANISM Homo sapiens

REFERENCE
 1 Krentz, R., Jimmer, S., Rost, S. and Hadwiger, P.
 Method for inhibiting the expression of a target gene.
 Patent: WO 02055693-A 81 18-JUL-2002;
 JOURNAL Ribopharma AG (DE)

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 VERSION AB037973.1 GI:10119773
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ORGANISM Homo sapiens CDNA to mRNA.
 Homo sapiens

REFERENCE
 1 (sites)
 Yamashta, T., Yoshio, M. and Itoh, N.
 Identification of a novel fibroblast growth factor, FGF-23,
 preferentially expressed in the ventrolateral thalamic nucleus of
 the brain

JOURNAL Biochem. Biophys. Res. Commun. 277 (2), 494-498 (2000)
 MEDLINE 20490027
 REFERENCE 2 (bases 1 to 756)
 Itoh, N.

AUTHORS Direct Submission
 Submitted (03-FEB-2000) Nobuyuki Itoh, Kyoto University, Graduate
 School of Pharmaceutical Sciences, Department of Genetic
 Biochemistry, Yoshida-Shimoadachi, Sakyo, Kyoto, Kyoto 606-8501,
 Japan (E-mail: itohn@pharm.kyoto-u.ac.jp, Tel: 81-75-753-4540,
 Fax: 81-75-753-4600)

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CDS

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 Db 661 AGTGAACCCATTAGAGGAGTGTCAAGGGCGGTGAGTGAACAGCAAGCTGGGGGAAGCGGC 720
 QY 867 CCGGAAGGCTGCGGCGCTTCCGCAAGTTGATCTAG 902
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RESULT 11
 AX235431 753 bp DNA linear PAT 11-SEP-2001
 LOCUS AX235431
 DEFINITION Sequence 1 from Patent WO0161007.
 ACCESSION AX235431
 VERSION AX235431.1 GI:15593931

KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 BUKARYOZA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 753)
 AUTHORS
 Luehthy, R., Yang, R., Suggs, S. and Sarosi, I.
 TITLE
 Fibroblast growth factor-23 molecules and uses thereof
 JOURNAL
 Patent: WO 0161007-A 1 23-AUG-2001;
 Amgen Inc. (US)

FEATURES
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sig_peptide 1..72
 BASE COUNT 158 a 250 c 211 g 134 t
 ORIGIN

Query Match 46.7%; Score 753; DB 6; Length 753;
 Best Local Similarity 100.0%; Pred. No. 7.2e-171;
 Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 ATGTTGGGGGGCCCGCTCAGGCTCTGGGTCTGTGCTTGTGACGCTGTGACATGAGC 206
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 Db 61 GTCTCAGAGCTATCCCAATGCTCCCACTGCTGGGCTCCAGCTGGGCTGATC 120
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 Db 121 CACCTGTACACAGCCACAGCCAGGACAGTACCACTGAGATCCACAAGAAATGGCCAT 180
 QY 327 GTGATAGGCGCCACCCCACTACAGCCATCTACAGTGCCTGTATGATCAGAGATGCT 386
 Db 181 GTGATAGGCGCCACCCCACTACAGCCATCTACAGTGCCTGTATGATCAGAGATGCT 240
 QY 387 GGCTTTGTGTGATTTACAGGTGTGATGAGAGAAATACCTCTGATGATTTCAAGAGC 446
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 QY 447 AACATTTTGGATCACTATTTCGACCCCGGAACTGAGGTTCCAAACACAGAGCTG 506
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 QY 567 GGGAGAGAGGCTTCTGTCAGAGGATGAAACCCCGGATCTCCAGTTCTGTCCGG 626
 Db 421 GGGAGAGAGGCTTCTGTCAGAGGATGAAACCCCGGATCTCCAGTTCTGTCCGG 480
 QY 627 AGGAAAGAGATCCCTTAATTCACTTCAACACCCCAATACAGGCGGCAACCCGAGC 686
 Db 481 AGGAAAGAGATCCCTTAATTCACTTCAACACCCCAATACAGGCGGCAACCCGAGC 540
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Db 601 CCGGCCCCGCGCTCTGTTCACAGAGCTCCCGAGCGCCGAGCAACAGCCCATGCGC 660
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Db 721 CCGGAAGGCTGCGCGCCCTTGCCCAAGTTCATC 753

RESULT 12
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DEFINITION Sequence 3 from Patent WO0149740.
ACCESSION AX191709
VERSION AX191709.1 GI:15209884
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 753)
AUTHORS Conklin,D.C.
TITLE Novel fgf homolog zfgf12
JOURNAL Patent: WO 0149740-A 3 12-JUL-2001;
ZymoGenetics, Inc. (US)
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/note="degenerate sequence"

BASE COUNT 108 a 90 c 132 g 94 t 329 others
ORIGIN
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Best Local Similarity 56.3%; Pred. No. 1,4e-116;
Matches 424; Conservative 180; Mismatches 149; Indels 0; Gaps 0;

Qy 147 ATGTGAGGGGCGCGCTCAGAGCTGTGGCTGTGGCTGTGGAGCGTGTGAGCATGAGC 206
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Qy 207 GTGCTCAGAGCTATCCCAATGCTCCCACTGCTCGGCTCCAGCTGGGGGTGCTGATC 266
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Qy 267 CACCTGTACACAGCAGCAGCAGGAGAGCAGTACCACTGTGAGTCAACAAGATGGCCAT 326
Db 121 CACCTGTACACAGCAGCAGCAGGAGAGCAGTACCACTGTGAGTCAACAAGATGGCCAT 180
Qy 327 GTGAGTGGGGGAGCCCATCTACAGCATCTACAGTCCCTGATGATCAATCAGAGATGCT 386
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Qy 447 AACATTTTGGATCACTATTTGAGCCCGAGAACTGCAAGTTCACAACAGACGCTG 506
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Qy 507 GAAAGAGGATGAGAGCTCTACCTCTCTCATGATCACTTCTGCTGCTGAGTGGCGCG 566
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Qy 567 GCGAAGAGAGCTTCCGCGAGGATGAGACCCCGCTACTCCCGAGTCTCTGCTCCCGG 626
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Db 721 CCGGAAGGCTGCGCGCCCTTGCCCAAGTTCATC 753

RESULT 13
AF263536 1559 bp mRNA linear ROD 14-DEC-2000
LOCUS Mus musculus FGF23 (Fgf23) mRNA, complete cds.
DEFINITION AF263536
ACCESSION AF263536
VERSION AF263536.1 GI:9964289
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 1559)
AUTHORS White,K.E., Evans,W.E., O'Riordan,J.L.H., Speer,M.C., Econs,M.J.,
Lorenz-Deplieux,B., Grabowski,M., Mellinger,T. and Strom,T.M.
TITLE Autosomal dominant hypophosphataemic rickets is associated with
mutations in FGF23
JOURNAL Nat. Genet. 26 (3), 345-348 (2000)
MEDLINE 20517346
PUBMED 11062477
REFERENCE 2 (bases 1 to 1559)
AUTHORS Strom,T.M.
TITLE Direct Substitution
JOURNAL Submitted (03-MAY-2000) Medizinische Genetik, Goethestr. 29,
Muenchen 80336, Germany
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BASE COUNT 347 a 457 c 405 g 350 t
ORIGIN
Query Match 28.4%; Score 457.4; DB 10; Length 1559;
Best Local Similarity 73.0%; Pred. No. 1.8e-99;
Matches 602; Conservative 0; Mismatches 221; Indels 2; Gaps 1;

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Qy 219 TATCCAGATGCTCCCGCACTGCTGGCTCCGAGTGGGGTGGCTGATCCACTCTTACACA 278

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Qy 459 TCACATATTTGACCCGAGAACTGAGAGTTCACACAGCAGCAGTGAAGAAAGCGGTAC 518

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Db 489 TTTCACCCGGGACCAACCCGCGCTTCTCCAGTTCCTGTGCTGGAGAGAAAGATC 548

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Db 609 CCGAGCGGAGCCCGCTTGAACGCTGTAAGCCCGGCGCGCGAGTGAACCCGCGCGCGGCG 668

Qy 759 TCTCTTTCACAGAGCTCCCGAGCCCGAGAGACACAGCCGATGGCAGTGAACCCATTA 818

Db 669 TCTCTCTCTCGAGAGCTCGAGCGAGCGAGAGAGTGGCCCGCAGCAGCAGATCTCTG 728

Qy 819 GGGGTGTGATGAGGGGGGTGAGTGAACAGCAAGCTGGGGAGACGGGCCCGAGAGCTGC 878

Db 729 GGGGTGTGATGAGGGGGGTGAGTGAACAGCAAGCTGGGGAGACGGGCCCGAGAGCTGC 788

Qy 879 CGCCCTTTCGAGGATCTTCTGAGGCTGGTGAAGAGGCGACCCCTC 923

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RESULT 14

AB078777 756 bp mRNA linear ROD 26-JAN-2002

LOCUS AB078777

DEFINITION Rattus norvegicus FGF23 mRNA for fibroblast growth factor 23.

ACCESSION AB078777

VERSION AB078777.1 GI:18376670

KEYWORDS

SOURCE Rattus norvegicus cDNA to mRNA.

ORGANISM Rattus norvegicus

REFERENCE 1 Itoh, N.

AUTHORS Rattus norvegicus fgf23

TITLE Published Only in Database (2002)

JOURNAL 2 (bases 1 to 756)

AUTHORS Itoh, N.

TITLE Direct Submission

JOURNAL Submitted (24-JAN-2002) Nobuyuki Itoh, Kyoto University Graduate School of Pharmaceutical Sciences, Department of Genetic Biochemistry, Yoshida-Shimosadachi, Sakyo, Kyoto 606-8501, Japan (E-mail: itohnobu@pharm.kyoto-u.ac.jp, Tel: 81-75-753-4540, Fax: 81-75-753-4600)

FEATURES

Location/Qualifiers

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/db_xref="taxon:10116"

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BASE COUNT 144 a 257 c 219 g 136 t

ORIGIN

Query Match 27.8%; Score 448.8; DB 10; Length 756;

Best Local Similarity 74.6%; Pred. No. 1.9e-97;

Matches 564; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

Qy 147 ATGTGGGGGCGCGCTCAGGCTGTGGTCTGTGCGAGCGCTGACAGATGAGC 206

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Qy 207 GTTCCTAGAGCCTATCCATGCTCCCACTGCTGCTGCGCTGAGCTGGGCTGATC 266

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Qy 267 CACTGTACACAGCCAGACAGACAGACAGCTTACCTGCAATGCCAAGATGGCCAT 326

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Qy 327 GTGATGGGCAAGCCATGACACATCTACAGTCCCTGATGATGATGATGATGATGATGATG 386

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Qy 507 GAAACGGGTAGAGCTTACACACTCTCTCACTTCTGCTGCTGCTGCTGCTGCTGCTG 566

Db 361 GAAACGGGTAGAGCTTACACACTCTCTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 420

Qy 567 GCGAAGAGACCTTCTGCGAGAGAGAGACCCAGCCGCTATCCCAAGTTCCTGTCGCG 626

Db 421 TCCAGAGCAGATTTTCAAGCCGCTGACCAACCGCGCGCTTCTGCGAGTTCCTGTCGCG 480

Qy 627 AGGAAGAGATCCCTTATATCTTCAACACCCCATACACAGCGGAGACACCCGAGC 686

Db 481 AGGAAGAGATCCCTTATATCTTCAACACCGCGCGCTTCTGCGAGTTCCTGTCGCG 540

Qy 687 GCGAGAGACACTCGAGCGGAGACCCCTGGAAGCTGGAAGCCCGGAGCGGAGTACC 746

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Qy 747 CCGGCGCGCGCTCTGTTCAAGAGCTCCGAGCGCGGAGAGACACCGCGATGGCC 806

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:52 ; Search time 84 Seconds

(without alignments)
615,688 Million cell updates/sec

Title: US-09-901-938-2

Perfect score: 1360

Sequence: 1 MGARLRMLVCAICVCSMS.....VNTHAGTGPEGCRPPAKFI 251

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
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- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvlnus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	181.5	13.3	245	11	Q8R5L9
5	158	11.6	196	13	Q9YH31
6	157	11.5	124	13	Q90X05
7	150.5	11.1	111	13	Q90X01
8	149.5	11.0	218	11	Q8V181
9	147.5	10.8	192	11	Q9ERW3
10	147.5	10.8	245	11	Q8V181
11	146.5	10.8	208	6	Q95K97
12	146	10.7	206	13	Q9YH31
13	144	10.6	211	11	Q8R5L9
14	143.5	10.6	212	13	Q42407
15	143	10.5	201	13	Q80G59
16	142	10.4	191	13	Q9DRC9

17	141	10.4	111	13	Q90Y71
18	140.5	10.3	199	13	Q9A1A3
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22	139.5	10.3	208	11	Q8R5L5
23	137.5	10.1	253	13	Q9A1A5
24	136.5	10.0	247	11	Q8R5L7
25	134	9.9	237	13	Q9A1A6
26	132.5	9.7	195	11	Q8R5L6
27	132	9.7	213	6	Q9N1B9
28	132	9.7	302	11	Q9C5X5
29	130.5	9.6	212	11	Q9C5T9
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31	130	9.6	207	11	Q9E5L8
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34	128	9.4	185	11	Q9ERN5
35	128	9.4	166	6	Q95L47
36	127	9.3	134	13	Q90X03
37	127	9.3	170	11	Q60487
38	127	9.3	181	11	Q924B4
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ALIGNMENTS

RESULT 1

Q8V182 PRELIMINARY; PRT; 251 AA.

AC Q8V182;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Fibroblast growth factor 23.
GN FGF23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Rattus norvegicus fgf23.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078777; BAB84108.1; -
DR InterPro; IPR002209; HB/F_growthfact.
DR Pfam; PF00167; FGF_1.
DR Prodom; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF_1.
DR SQUENCE 251 AA; 27911 MW; 35A229E1B390593 CRC64;

Query Match 71.9%; Score 978; DB 11; Length 251;
Best local Similarity 71.7%; Pred. No. 3.9e-86;
Matches 180; Conservative 26; Mismatches 45; Indels 0; Gaps 0;

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RESULT 2

Q8V180 PRELIMINARY; PRT; 208 AA.
 AC Q8V180;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
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 GN FGF21.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Itoh N.;
 RT "Rattus norvegicus FGF21,"
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078901; BAB84289.1;
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF_1.
 DR PRINTS; PR00262; ILHBGF.
 DR Prodom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF_1.
 SQ SEQUENCE 208 AA; 22857 MW; D232445902CDB8EA CRC64;

Query Match 17.6%; Score 239; DB 11; Length 208;
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 Matches 67; Conservative 39; Mismatches 73; Indels 36; Gaps 8;

QY 8 LWCALCSVCSMSVLRAPV-NASPLGSSWGLI--HLYTATARNV-YHLOIHKNGHV 61
 Db 13 LWCALCSVCSMSVLRAPV-NASPLGSSWGLI--HLYTATARNV-YHLOIHKNGHV 61
 QY 62 DGAPHQITYSALMIRSEDAGFVITGVMSRRLCMDFRGNIFGSHYDPENCRFQHOTLE 121
 Db 71 VGTARHPESLLEIKALKPVGVIQILGVASRFLCQDPGTLGSPHFDPEACSFRELLLK 130
 QY 122 NGQDVYSPQYHFLVSL-----GRAKAFLEPGMNPFPYSGFLSRNEIPLIHEN 170
 Db 131 DGNVYVSEAHGLPLRLPOKDSOPATRGVRLPMLPHEPHEQO---PGVLP----- 181
 QY 171 TPIPRHTRSAEDSERDPLVNLKPRAMTPAPAS 205
 Db 182 -PEP-----PDVGSDDPLSMVEPLQGRSPSYAS 208

RESULT 3
 Q9DDNO PRELIMINARY; PRT; 227 AA.
 AC Q9DDNO;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Fibroblast growth factor 19.
 GN FGF-19.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 NCBI_TaxID=9031;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20564778; PubMed=11110663;
 RA Lader R.K., Anake K.U., Gurney A.L., Schoenwolf G.C.,
 RA Francis-West P.H.;
 RT "Identification of Synergistic Signals Initiating Inner Ear
 RT Development,"
 RL Science 290:1965-1968 (2000).
 DR EMBL; AF315355; AAC39478.1;
 DR HSSP; P09038; IIRG.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF_1.
 DR PRINTS; PR00262; ILHBGF.
 DR Prodom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF_1.
 DR PROSITE; PS00247; HBGF_FGF; UNKNOWN 1.
 SQ SEQUENCE 227 AA; 24568 MW; 875D76FBFD09F8E2 CRC64;

Query Match 14.3%; Score 194.5; DB 13; Length 227;
 Best Local Similarity 29.9%; Pred. No. 9.7e-11;
 Matches 67; Conservative 30; Mismatches 104; Indels 23; Gaps 7;

QY 3 GARLRLWVLCVCSMSVLRAPV-NASPLGSSWGLIHLTYTATARNVYH-----LOI 55
 Db 10 GARLRLWVLCVCSMSVLRAPV-NASPLGSSWGLIHLTYTATARNVYH-----LOI 55
 QY 56 HKXNDVGCAPHQITYSALMIRSEDAGFVITGVMSRRLCMDFRGNIFGSHYDPENCRF 115
 Db 68 GGDGRVAVGSSQSPQSLLEIRAVAVRTVAIKGVSSRYLCMDXEGRLHGLQSLIEDCSF 127
 QY 116 QHOTLENGYDVYSPQYHFLVSLGRAR-RAFLPGMNPFPYSGFLSRNEIPL----- 166
 Db 128 EEFIRPDGINVYSSKKTGISVLSAKQOFKQDPLPSHFLPMINTVPEVTDFGEY 187
 QY 167 -IHFNTPIPRRHTRSAEDSERDPLVNLKPRAMTPAPASCOSQ 209
 Db 188 GDVSGAFEPVYSSPLETDS-MDPFGI---TSKLSPVKSPSPQK 227

RESULT 4

Q8R5L9 PRELIMINARY; PRT; 245 AA.
 AC Q8R5L9;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE FGF3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Itoh N.;
 RT "Rattus norvegicus FGF3 mRNA,"
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB079262; BAB84564.1;
 SQ SEQUENCE 245 AA; 27150 MW; C9305D307E7D0648 CRC64;

Query Match 13.3%; Score 181.5; DB 11; Length 245;
 Best Local Similarity 29.0%; Pred. No. 1.9e-09;
 Matches 62; Conservative 29; Mismatches 86; Indels 37; Gaps 8;

QY 42 LYTATARNVYHLOIHKNGHVDGAPHQITYSALMIRSEDAGFVITGVMSRRLCMDFRGN 101
 Db 48 LYCAT---KTHQLHSGKNGSLNSAYSILFTYVEGVVAIKGLFGRYLANKRGR 104
 QY 102 IFGSHYDPENCRFQHOTLENGYDVYSPQYHFLVSLGRARAFLEPGMNP----- 152
 Db 105 LVASEHYNAE-CEFVERIHGLGVNTYASRLYRTGPGPARQ--PGAGRPMVVSNGKG 161
 QY 153 -PYSGFLSRNEIPLIHNTPIR-----RHTRSAEDSERDPLVNLKPRAMTPAPA 204

DB 162 RPRRGFTRRRTQKSLF-----LPRLVGHKHGMWRLILGSGPQAPGESSGQROR----- 211

QY 205 SCGEPLPSAEDNSPMASDPLGVNRCGRVNTAAG 238

DB 212 --RQKQSPGDHGMHEHLPVATTSAGLDT--GG 241

RESULT 5

Q9YH31 PRELIMINARY; PRT; 196 AA.

AC Q9YH31; 01-MAY-1999 (T-EMBLrel. 10, Created)

DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Putative fibroblast growth factor-4.

OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;

OC Notophthalmus.

OX NCBI_TaxID=8316;

RN NCBI_TaxID=8316;

RP SEQUENCE FROM N.A.

RA Wei Y.;

RT "Putative Newt Fibroblast Growth Factor-4.";

RU Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U76998; AAC98812.1; -

DR HSSP; P09038; 1BFP.

DR InterPro; IPR001064; Crystallin.

DR InterPro; IPR002209; HB/F_growthfact.

DR InterPro; IPR002348; IL1_HBGF.

DR Pfam; PF00167; FGF_1.

DR PRINTS; PR00262; IL1HBGF.

DR ProDom; PD000831; HB/F_growthfact; 1.

DR SMART; SM00442; FGF_1.

DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

DR PROSITE; PS00247; HBGF_FGF; I.

SQ SEQUENCE 196 AA; 22033 MW; AC4688CD989C6EAF CRC64;

Query Match 11.6%; Score 158; DB 13; Length 196;

Best Local Similarity 34.8%; Pred. No. 2.6e-07;

Matches 39; Conservative 16; Mismatches 41; Indels 16; Gaps 3;

QY 51 YHLOIHNKGVHDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLCDPRGNIFGSHYFDP 110

DB 84 FHQVLPDGIHGHSHSRSLLEISPERGVCMFVGOSLFLANMSKGLPESKTFSD 143

QY 111 ENCRFQHTLENGVDVYHS---PQHFVLSGRAKA-----FLP 147

DB 144 E-CKFKEMLPNNYNAYESWRYPGYIALSKNGRAKKGNKVPMTVTYHFLP 194

RESULT 6

Q90X05 PRELIMINARY; PRT; 124 AA.

AC Q90X05; 01-DEC-2001 (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Fibroblast growth factor 4 (Fragment).

OS Ambystoma mexicanum (Axolotl).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

OC Ambystoma.

OX NCBI_TaxID=8296;

RN NCBI_TaxID=8296;

RP SEQUENCE FROM N.A.

RX MEDLINE=21439472; PubMed=1155861;

RA Christensen R.N.; Weinstein M.; Tassava R.A.;

RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning

and semi-quantitative RT-PCR expression studies.";

DT J. Exp. Zool. 290:529-540(2001).

DR EMBL; AF360984; AAL16957.1; -

DR InterPro; IPR001064; Crystallin.

DR InterPro; IPR002209; HB/F_growthfact.

DR Pfam; PF00167; FGF_1.

DR ProDom; PD000831; HB/F_growthfact; 1.

DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 124 AA; 14161 MW; 919CE10E9F6CEB3 CRC64;

Query Match 11.5%; Score 157; DB 13; Length 124;

Best Local Similarity 35.3%; Pred. No. 1.9e-07;

Matches 41; Conservative 18; Mismatches 47; Indels 10; Gaps 4;

QY 51 YHLOIHNKGVHDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLCDPRGNIFGSHYFDP 110

DB 12 FHQVLPDGIHGHSHSRSLLEISPERGVCMFVGOSLFLANMSKGLPESKTFSD 143

QY 111 ENCRFQHTLENGVDVYHSPOYH---FLVSLGRAKA--FLPMNPPYSQFLSR 160

DB 71 BECKFKETLLANNYNAYESWRYPGYIALSKNGRTKRGNEVSPMTN--VTHFLPR 123

RESULT 7

Q90X01 PRELIMINARY; PRT; 111 AA.

AC Q90X01; 01-DEC-2001 (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Fibroblast growth factor 4 (Fragment).

OS Ambystoma maculatum (spotted salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;

OC Ambystoma.

OX NCBI_TaxID=43114;

RN NCBI_TaxID=43114;

RP SEQUENCE FROM N.A.

RX MEDLINE=21439472; PubMed=1155861;

RA Christensen R.N.; Weinstein M.; Tassava R.A.;

RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning

and semi-quantitative RT-PCR expression studies.";

DT J. Exp. Zool. 290:529-540(2001).

DR EMBL; AF360988; AAL16961.1; -

DR InterPro; IPR001064; Crystallin.

DR InterPro; IPR002209; HB/F_growthfact.

DR Pfam; PF00167; FGF_1.

DR ProDom; PD000831; HB/F_growthfact; 1.

DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.

FT NON_TER 1

SQ SEQUENCE 111 AA; 12607 MW; 4A3A52ED39001057 CRC64;

Query Match 11.1%; Score 150.5; DB 13; Length 111;

Best Local Similarity 36.1%; Pred. No. 6.8e-07;

Matches 35; Conservative 16; Mismatches 41; Indels 5; Gaps 2;

QY 51 YHLOIHNKGVHDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLCDPRGNIFGSHYFDP 110

DB 12 FHQVLPDGIHGHSHSRSLLEISPERGVCMFVGOSLFLANMSKGLPESKTFSD 143

QY 111 ENCRFQHTLENGVDVYHSPOYH---FLVSLGRAKA 143

DB 71 BECKFKETLLANNYNAYESWRYPGYIALSKNGRTKRGNEVSPMTN 107

RESULT 8

Q8V181 PRELIMINARY; PRT; 218 AA.

AC Q8V181; 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Fibroblast growth factor 15.
 GN FGF15.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Itoh N.;
 RT "Rattus norvegicus FGF15";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB078900; BAB84298.1; -
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 SQ SEQUENCE 218 AA; 25207 MW; ED89684B5307C58 CRC64;

Query Match 11.0%; Score 149.5; DB 11; Length 218;
 Best Local Similarity 26.3%; Pred. No. 2e-06;
 Matches 51; Conservative 26; Mismatches 80; Indels 37; Gaps 6;

QY 30 PLTSSWGGLHLVATARNSTY---HIOIKNGHVDGAPHOTIYSALMIRSEDAGFVI 85
 DB 40 PLFLYMGKIRLQVLYAGFYNSCFIRISDGSVDCEBDONENLLEFPAVALKTAI 99
 QY 86 TGVMSRYLQMDFRGNIFGSHYFPCNCRFOHQLTENGVDYHSPQYFLVSLGRK-RA 144
 DB 100 KDVSYSVRLCWSADOKIYGLIRYSESDCTFPEMDCLQYNGRSKHLHIIIFAKRE 159
 QY 145 FLPGMNPPEYQFLSRNREIPLIH-----FMTPIPRHTRSAEDSERDPL 190
 DB 160 QLOQOKP-----SNFIPFIHRSFPESTDQLRSKNFSLPL-----ESDS-MDPF 201
 QY 191 NVLKRPAWTPAPA 204
 DB 202 RMVEDVHLVKSFS 215

RESULT 9

Q9ERM3 PRELIMINARY; PRT; 192 AA.
 AC Q9ERM3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Fibroblast growth factor 13.
 GN FGF13.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=DORSAL ROOT GANGLION; Guo C., Chen Z., Han Z., Zhang X.;
 RT "Rattus norvegicus fibroblast growth factor 13";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF271786; AAG15492.1; -
 DR HSP; P31371; I682.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 SQ SEQUENCE 192 AA; 21604 MW; 7736A3671677B263 CRC64;

Query Match 10.8%; Score 147.5; DB 11; Length 192;

Best Local Similarity 25.1%; Pred. No. 2.6e-06;
 Matches 54; Conservative 31; Mismatches 81; Indels 49; Gaps 10;

QY 37 GGLHLVATARNSTYHIOIKNGHVDGAPHQ-TYSLMIRSEBAGVITGVMSRYLC 95
 DB 15 GIVTKLY---SRQYHQLQLODGTIDGTKDESDTYTLFNLIPVGLRVVALQGVTKLYLA 71
 QY 96 MDPFGNIFGSHYFPCNCRFOHQLTENGVDYHSPQYFLVSLGRAKRAFLPGKPPYS 155
 DB 72 MNSRGYLYTSHFTPE-CKRESYFENYVYYSMTIR---QQSGRGWTLGIN----- 121
 QY 156 QFLSRNEIPLIHNTPIPRHTRSAEDSERDPLNVLKPRARWTPAPASCSQ-ELPSAE 214
 DB 122 ---KEGEI-----MKGNHYKKN-----KPAARLPKPLKVMYKEPSLH 157
 QY 215 D-----NSPMASDPL-GVARGGRVNTAGCT 239
 DB 158 DLTEFSRSGSGTPTKRSRVSGLNGKSMSHNEST 192

RESULT 10

Q9VCY9 PRELIMINARY; PRT; 245 AA.
 AC Q9VCY9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Fibroblast growth factor 13.
 GN FGF13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RT TISSUE=RETINA;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018238; AAI18238.1; -
 DR MGD; MGI:109178; Fgf13.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 SQ SEQUENCE 245 AA; 27587 MW; 5B96D41AC3A3DF78 CRC64;

Query Match 10.8%; Score 147.5; DB 11; Length 245;
 Best Local Similarity 25.1%; Pred. No. 3.6e-06;
 Matches 54; Conservative 31; Mismatches 81; Indels 49; Gaps 10;

QY 37 GGLHLVATARNSTYHIOIKNGHVDGAPHQ-TYSLMIRSEBAGVITGVMSRYLC 95
 DB 68 GIVTKLY---SRQYHQLQLODGTIDGTKDESDTYTLFNLIPVGLRVVALQGVTKLYLA 124
 QY 96 MDPFGNIFGSHYFPCNCRFOHQLTENGVDYHSPQYFLVSLGRAKRAFLPGKPPYS 155
 DB 125 MNSRGYLYTSHFTPE-CKRESYFENYVYYSMTIR---QQSGRGWTLGIN----- 174
 QY 156 QFLSRNEIPLIHNTPIPRHTRSAEDSERDPLNVLKPRARWTPAPASCSQ-ELPSAE 214
 DB 175 ---KEGEI-----MKGNHYKKN-----KPAARLPKPLKVMYKEPSLH 210
 QY 215 D-----NSPMASDPL-GVARGGRVNTAGCT 239
 DB 211 DLTEFSRSGSGTPTKRSRVSGLNGKSMSHNEST 245

RESULT 11

Q95K97 PRELIMINARY; PRT; 208 AA.
 ID Q95K97

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AC Q95K97;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 23.5 kDa protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MEDULLA OBLONGATA;
RA Oseada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB063051; BAB60779.1; -.
DR InterPro; IPR002209; HB/F_growthfact.
DR Pfam; PF00167; FGF, 1.
DR ProDom; PD000831; HB/F_growthfact; 1.
DR PROSITE; PS00247; HBGF_FGF, UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 208 AA; 23466 MW; 0766A787609B3661 CRC64;

Query Match 10.8%; Score 146.5; DB 6; Length 208;
Best Local Similarity 32.0%; Pred. No. 3.7e-06;
Matches 39; Conservative 20; Mismatches 54; Indels 9; Gaps 4;

QY 51 YHLOIHKNGHVDGAPHQRT-YSALMIRSDAGFVITGVMSRRYLQMPFRGNI FGSHPYD 109
DB 88 YFLIEKNGKXVSGTKKCNPSYILSTVETGVAVKAINSYVLAAMKGLYSKKEFN 147
QY 110 PENCRFQHOTLENGDVHSPQYHFLVSLGRAKRAFLPGMNPSPVSOPLSRNE----IP 165
DB 148 -NDCKLKRIRKENGNYNTASFRWQ--HNGROMYVALMGKAPRGQKTRKRNTSAHFLP 203
QY 166 LI 167
DB 204 MV 205

RESULT 12
Q9YGD8
ID Q9YGD8 PRELIMINARY; PRT; 206 AA.
AC Q9YGD8;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Fibroblast growth factor 6-related protein.
GN FGF6.
OS Oncomorphus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncomorphus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99096461; Pubmed=9878802;
RA Rescan P.Y.;
RT "Identification of a fibroblast growth factor 6 (FGF6) in a non-
RT mammalian vertebrate: Continuous expression of FGF6 accompanies muscle
RT fiber hyperplasia."
RL Biochim. Biophys. Acta 1443:305-314(1998).
DR EMBL; Y16850; CAAT6422.1; -.
DR HSSP; P31371; IGB2.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; ILL_HBGF.
DR Pfam; PF00167; FGF, 1.
DR PRINTS; PR00262; ILLHBGF.
DR ProDom; PD000831; HB/F_growthfact; 1.

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DR SMART; SM00442; FGF, 1.
DR PROSITE; PS00225; CRYSTALLIN BTAGAMMA, UNKNOWN_1.
DR PROSITE; PS00247; HBGF_FGF, 1.
SQ SEQUENCE 206 AA; 23375 MW; BB883328F17EB6E4 CRC64;

Query Match 10.7%; Score 146; DB 13; Length 206;
Best Local Similarity 31.2%; Pred. No. 4e-06;
Matches 35; Conservative 20; Mismatches 41; Indels 16; Gaps 3;

QY 51 YHLOIHKNGHVDGAPHQRTYSALMIRSDAGFVITGVMSRRYLQMPFRGNI FGSHPYD 110
DB 94 YHLOVLPDGRINGTNGNQSILSTYERGVSLYGRSELPVAMNSRGRLYGTTHFD 153
QY 111 ENCRFQHOTLENGDVHSPQYH---FLVSLGRAKRA-----FLP 147
DB 154 E-CRFRSEMLPNNVAVAYESSVYRGSYIALNKGRLKKKATYMTATVTHFLP 204

RESULT 13
Q8R4X0
ID Q8R4X0 PRELIMINARY; PRT; 211 AA.
AC Q8R4X0;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Fibroblast growth factor-like factor-4D (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu C., Dib-Hajj S.D., Maxman S.G.;
RT "Fibroblast growth factor homologous factor-4D."
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF348523; AAL83904.1; -.
FT NON TER 1
SQ SEQUENCE 211 AA; 23346 MW; 046C18019C63BA3 CRC64;

Query Match 10.6%; Score 144; DB 11; Length 211;
Best Local Similarity 24.7%; Pred. No. 6.5e-06;
Matches 54; Conservative 39; Mismatches 78; Indels 48; Gaps 11;

QY 9 WVCAICGVCSWVLRAYVNASPLLGSSWGLIHLTYTARSYHLOIHKNGHVDG----A 64
DB 11 WV--LQCIQKSLKK--KNKPTDPQKGIYTRLY---CRGYVLQWMPDGLGTYKDS 62
QY 65 PHQTYTALMIRSDAGFVITGVMSRRYLQMPFRGNI FGSHPYD PENCRFQHOTLENGY 124
DB 63 TNSLTPNLIPV---GLAVVALQGVKTGLTYAMNGEGLYPSLFTPE-CRKESVFNYY 118
QY 125 DVHSPQYHFLVSLGRAKRAFLPGMN-----PPYSQPLSRNEIPLIHENT 171
DB 119 VIYSMLYR-----QOESGRAWFLGLNREGQWKNRVKTPAHPLPKLEVAM--YRE 172
QY 172 PIPRRHRSADDSERPLNVLKRAAMTPAPASQSEL 210
DB 173 P-----SLHDVGE-----TVPKAGVTPSKSTYSAGAI 198

RESULT 14
O42407
ID O42407 PRELIMINARY; PRT; 212 AA.
AC O42407;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Fibroblast growth factor 10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

```

RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9730690; PubMed=9187149;
 RA Ohuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y.,
 RA Yoshioka H., Kuwana T., Nohno T., Yamaaki M., Itoh N., Noji S.,
 RT "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
 RT of the chick limb bud through interaction with FGF8, an apical
 RT ectodermal factor."
 RL Development 124:2235-2244(1997).
 DR EMBL: D86333; BAA24945.1; -
 DR HSSP: P31371; IG82
 DR InterPro: IPR002209; HB/F_growthfact.
 DR Pfam: PF00167; FGF, 1.
 DR ProDom: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF, 1.
 SQ SEQUENCE 212 AA; 23631 MW; AB4C0B32C72A0D90 CRC64;

Query Match 10.6%; Score 143.5; DB 13; Length 212;
 Best Local Similarity 31.9%; Pred. No. 7.3e-06;
 Matches 38; Conservative 19; Mismatches 41; Indels 21; Gaps 5;

QY 49 NSYHQLHKNQGVDAFPHQT-YSLMIRSEDAGFVITGMSRRYLQMDPRGNIQSGSHY 107
 DB 90 NKYFLKLEKNGKVGSTKKNCPFSLLETVEIGVAVKSIKSNYYLANKKGVYSKE 149
 QY 108 FDPENCRFHQTLNGVDVY-----HSPQYHFLVSLGR-AKRA-----FLP 147
 DB 150 FN-SDCKLKERIENGVTYVSLMKHNGRQMFVNLNGRGATKGQKTRKNTSAHFLP 207

RESULT 15

Q8QG59 PRELIMINARY; PRT; 201 AA.
 AC Q8QG59;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Fibroblast growth factor 10.
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21826199; PubMed=11836784;
 RA Christensen R.N., Weinstein M., Tassava R.A.;
 RT "Expression of fibroblast growth factors 4, 8, and 10 in limbs,
 RT flanks, and blastemas of Ambystoma."
 RL Dev. Dyn. 223:193-203(2002).
 DR EMBL: AY034453; AAKS9700.1; -
 SQ SEQUENCE 201 AA; 22994 MW; 89EAE1B61806A6F57 CRC64;

Query Match 10.5%; Score 143; DB 13; Length 201;
 Best Local Similarity 27.5%; Pred. No. 7.6e-06;
 Matches 47; Conservative 25; Mismatches 79; Indels 20; Gaps 6;

QY 6 LRLWVCAICSYC-----SMVLRVAPNAPPLG-----SSWGLIHLYTATANSYHLQ 54
 DB 21 LLLWVSCISVTCHDLARMDLSPEVANSVPVGRQVRSYKHLGVDVRLRLLCVTNYFLK 80
 QY 55 IHKNGHVDGAH-QTIYSALMIRSEDAGFVITGMSRRYLQMDPRGNIQSGSHYDPENC 113
 DB 81 IDADGKVGSTTKVDCPFYSMEITSVDVGIVAVKGVSNYYLANKKGVYSRREFTD-C 139
 QY 114 RFOHQTLENGVDVYHSPQYHFLVSLGRARAF--LPGNNPPYSOFLSRN 162
 DB 140 KTKRMENKNTYASYKMRH-----KQRMFVALNGKGTFRGQKTRKN 185

Search completed: May 23, 2003, 07:45:45
 Job time : 86 secs

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:52 ; Search time 25 Seconds

(without alignments)
416,422 Million cell updates/sec

Title: US-09-901-938-2

Sequence: 1360
1 MLGARLRMLWCALCSCVCSMS.....VNTAGTGEGCRPPAKFI 251

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1360	100.0	251 1	FGFN_HUMAN
2	961	70.7	251 1	Q9GZV9 homo sapien
3	241	17.7	210 1	FGFN_MOUSE
4	222.5	16.4	209 1	FGFL_MOUSE
5	207	15.2	216 1	FGFL_HUMAN
6	182.5	13.4	245 1	FGFJ_HUMAN
7	180.5	13.3	239 1	FGFJ_MOUSE
8	178.5	13.1	237 1	FGF3_HUMAN
9	176.5	13.0	266 1	FGF3_XENLA
10	171	12.6	264 1	FGF5_RAT
11	168.5	12.4	268 1	FGF5_MOUSE
12	167	12.3	220 1	FGF3_CHICK
13	159.5	11.7	256 1	FGF3_BRAE
14	155	11.4	192 1	FGFB_XENLA
15	151	11.1	187 1	FGFA_XENLA
16	147.5	10.8	245 1	FGFD_MOUSE
17	146.5	10.8	194 1	FGF4_MOUSE
18	146.5	10.8	208 1	FGF4_CHICK
19	146.5	10.8	208 1	FGFA_HUMAN
20	145.5	10.7	209 1	FGFA_MOUSE
21	144.5	10.6	245 1	FGFD_HUMAN
22	142	10.4	206 1	FGF4_BOVIN
23	141.5	10.4	208 1	FGF6_HUMAN
24	141.5	10.4	218 1	FGF6_MOUSE
25	138.5	10.2	208 1	FGF6_MOUSE
26	136.5	10.0	247 1	FGFE_MOUSE
27	135	9.9	247 1	FGFE_HUMAN
28	132.5	9.7	211 1	FGFK_HUMAN
29	132	9.7	207 1	FGFG_RAT
30	131.5	9.7	206 1	FGFA_HUMAN
31	131	9.6	202 1	FGF4_MOUSE
32	129	9.5	207 1	FGFG_HUMAN
33	128	9.4	194 1	FGF7_CANPA

34	128	9.4	194 1	FGF7_MOUSE	P36363 mus musculus
35	127	9.3	194 1	FGF7_PIG	Q9H198 sus scrofa
36	127	9.3	194 1	FGF7_SHEEP	P48808 ovis aries
37	127	9.3	243 1	FGFC_HUMAN	Q92912 homo sapien
38	126	9.3	194 1	FGF7_HUMAN	P21781 homo sapien
39	124.5	9.2	162 1	FGFM_MOUSE	Q96882 mus musculus
40	118.5	8.7	170 1	FGFM_HUMAN	Q9HCT0 homo sapien
41	118	8.7	208 1	FGF9_HUMAN	P31371 homo sapien
42	118	8.7	208 1	FGF9_MOUSE	P54130 mus musculus
43	118	8.6	154 1	FGF2_RAT	P36364 rattus norv
44	117	8.6	154 1	FGF2_RAT	P31309 rattus norv
45	116.5	8.6	154 1	FGF2_MOUSE	P15655 mus musculus

ALIGNMENTS

RESULT 1
ID FGFN_HUMAN STANDARD; PRT; 251 AA.
AC Q9GZV9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23) (Tumor-derived hypophosphatemia inducing factor).
GN FGF23 OR HYPF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=20490027; PubMed=11032749;
RA Yamashita T., Yoshioke M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23, preferentially expressed in the ventrolateral thalamic nucleus of the brain."
RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN [2]
RP SEQUENCE FROM N.A., VARIANTS ADHR Q-176; Q-179 AND W-179, AND VARIANTS M-239.
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorentz-DePietreux B., Grabowski M., Weisinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with mutations in FGF23.";
RL Nat. Genet. 26:345-348(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11344269;
RA Shimada T., Mizutani S., Muto T., Yoneya T., Hino R., Takeda S., Takeuchi Y., Fujita T., Fukumoto S., Yamashita T.;
RT "Cloning and characterization of FGF23 as a causative factor of tumor-induced osteomalacia."
RL Proc. Natl. Acad. Sci. U.S.A. 98:6500-6505(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- DISEASE: DEFECTS IN FGF23 ARE THE CAUSE OF AUTOSOMAL DOMINANT HYPOPHOSPHATEMIC RICKETS (ADHR). ADHR IS CHARACTERIZED BY LOW SERUM PHOSPHORUS CONCENTRATIONS, RICKETS, OSTEOALACIA, LEG DEFORMITIES, SHORT STATURE, BONE PAIN AND DENTAL ABSCESSES.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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DR EMBL; AB037973; BAB13477.1; -;
DR EMBL; AF263537; AAC09917.1; -;

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DR EMBL: AB047858; BAB55889.1; -
DR HSPB; P03968; IAF.
DR Genew; HGNC:3680; FGF23.
DR MIM; 605380; -
DR MIM; 193100; -
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF_1.
DR POSITE; PS00247; HBGF_FGF; FALSE_NEG.
KM Growth factor; Signal; Disease mutation; Polymorphism.
FT SIGNAL 1 24
FT CHAIN 25 251
FT VARIANT 176 176
FT VARIANT 179 179
FT VARIANT 179 179
FT VARIANT 179 179
FT VARIANT 239 239
FT VARIANT 239 239
SO SEQUENCE 251 AA; 27954 MW; 6093BD0CC50C2489 CRC64;

Query Match 100.0%; Score 1360; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 4e-116;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGARLRLMVCALCSVCSMSVLRAPNAPSPLLGSSWGLIHLTYTARNSYHLQIHKNKH 60
DB 1 MLGARLRLMVCALCSVCSMSVLRAPNAPSPLLGSSWGLIHLTYTARNSYHLQIHKNKH 60
QY 61 VDGAPHOTIYSALMIRSEDAGFVITGVMSRRYLCDMFRGNIFGSHYDPENCROHOTL 120
DB 61 VDGAPHOTIYSALMIRSEDAGFVITGVMSRRYLCDMFRGNIFGSHYDPENCROHOTL 120
QY 121 ENGVDVHSPQYHFLVLSIGAKRAFLPGMNPYPYQPLSRNRIPLIHNTPIPRRHTRS 180
DB 121 ENGVDVHSPQYHFLVLSIGAKRAFLPGMNPYPYQPLSRNRIPLIHNTPIPRRHTRS 180
QY 181 AEDSESDPLNLKPRRMTAPAPASCQELPSAEDNSPMASDPLGVVGRVNTHAGTG 240
DB 181 AEDSESDPLNLKPRRMTAPAPASCQELPSAEDNSPMASDPLGVVGRVNTHAGTG 240
QY 241 PEGCRPPAKFI 251
DB 241 PEGCRPPAKFI 251

RESULT 2
FGFN_MOUSE STANDARD; PRT; 251 AA.
AC 09ERG2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23).
GN FGF23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20450027; PubMed=11032749;
RA Yamaehita T., Yoshioka M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23, preferentially expressed in the ventrolateral thalamic nucleus of the brain."
RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN [2]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=BALB/c; TISSUE=Embryo;
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan T.J.H., Speer M.C., Reons M.J.,
RA Lorenz-Dejareux B., Grabowski M., Meltinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with mutations in FGF23."
RL Nat. Genet. 26:345-348(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE BRAIN AND THYMUS AT LOW LEVELS. IN BRAIN; PREFERENTIALLY EXPRESSED IN THE VENTROLATERAL THALAMIC NUCLEUS.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC -----
DR EMBL; AB037889; BAB13478.1; -
DR HSPB; AF263536; AAC09916.1; -
DR HSPB; P03968; IBAF.
DR MED; MG1:1891427; FGF23.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF_1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF_1.
DR POSITE; PS00247; HBGF_FGF; FALSE_NEG.
KM Growth factor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 251
FT VARIANT 251 251
SO SEQUENCE 251 AA; 27757 MW; 110C1F2C735DC360 CRC64;

Query Match 70.7%; Score 961; DB 1; Length 251;
Best Local Similarity 70.5%; Pred. No. 5.7e-80;
Matches 177; Conservative 25; Mismatches 49; Indels 0; Gaps 0;

QY 1 MLGARLRLMVCALCSVCSMSVLRAPNAPSPLLGSSWGLIHLTYTARNSYHLQIHKNKH 60
DB 1 MLGARLRLMVCALCSVCSMSVLRAPNAPSPLLGSSWGLIHLTYTARNSYHLQIHKNKH 60
QY 61 VDGAPHOTIYSALMIRSEDAGFVITGVMSRRYLCDMFRGNIFGSHYDPENCROHOTL 120
DB 61 VDGAPHOTIYSALMIRSEDAGFVITGVMSRRYLCDMFRGNIFGSHYDPENCROHOTL 120
QY 121 ENGVDVHSPQYHFLVLSIGAKRAFLPGMNPYPYQPLSRNRIPLIHNTPIPRRHTRS 180
DB 121 ENGVDVHSPQYHFLVLSIGAKRAFLPGMNPYPYQPLSRNRIPLIHNTPIPRRHTRS 180
QY 181 AEDSESDPLNLKPRRMTAPAPASCQELPSAEDNSPMASDPLGVVGRVNTHAGTG 240
DB 181 AEDSESDPLNLKPRRMTAPAPASCQELPSAEDNSPMASDPLGVVGRVNTHAGTG 240
QY 241 PEGCRPPAKFI 251
DB 241 ADRCRPPRPV 251

RESULT 3
FGFL_MOUSE STANDARD; PRT; 210 AA.
AC 09JUN1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21).
GN FGF21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RT Mismimura T., Nakatake Y., Konishi M., Itoh N.,
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
RT the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamano I.,
RA Saito T., Okazaki Y., Gojopori T., Bono H., Kaakawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombereis P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyoko-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- TISSUE SPECIFICITY: MOST ABUNDANTLY EXPRESSED IN THE LIVER, ALSO
CC EXPRESSED IN THE THYMUS AT LOWER LEVELS.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC -----
DR EMBL; AB025718; BAA9416.1; -
DR EMBL; AK007574; BAA25115.1; -
DR HSSP; P03968; IBAR.
DR MGD; MGI1861377; Fgf21.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
DR Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 210
FT SEQUENCE 210 AA; 22327 MW; AB02NABA6477BE6F0 CRC64;
SQ
Query Match 17.7%; Score 241; DB 1; Length 210;
Best Local Similarity 32.3%; Pred. No. 7.9e-15;
Matches 71; Conservative 38; Mismatches 71; Indels 40; Gaps 8;
QY 6 LRLVWVLCVCSMSVLRAY--PNASPLLGSSWGGLI---HLVYATARN--YHLQIHNG 59
DB 11 LGLMVRLLAVFLGLVQVAVPIPDSSPL--QFGQVQRRLVYTDQDTFAHLEINEDG 68
QY 60 HVGGAHQITVYSLMISSEDAAGFVITGVMSRRYLCDPFRNITGSHYFDPENCRFQHOT 119
DB 69 TVVGAARHSBPSLLEALKRGVILGLVAKSRFLCOOPDALYGSHPFPEACSFRELL 128

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QY 120 LENGVDVHSPQYHFL-----VSLGRAKAFILPGMNPFPYSQFLSRNEIP 165
DB 129 LEDGVNVYQS--BAHGLPLRLPQKDS PNDATSWGVRLPMGLLHEPDQ----- 178
QY 166 LIHFNTPIPRHTRSAEDSERDPPLNVLKPRAPMAPAS 205
DB 179 -AGFLPPER-----PDVGSDDLMTWYPLQGRSPSTAS 210
RESULT 4
FFGL_HUMAN STANDARD; PRT: 209 AA.
ID FFGL_HUMAN
AC Q9NSA1.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21).
GN FGF21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Mismimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
RT the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB021975; BAA9415.1; -
DR HSSP; P03968; IBAR.
DR HSSP; HGNC:3678; FGF21.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
DR Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 209
FT SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;
SQ
Query Match 16.4%; Score 222.5; DB 1; Length 209;
Best Local Similarity 30.8%; Pred. No. 3.7e-13;
Matches 68; Conservative 36; Mismatches 70; Indels 47; Gaps 9;
QY 8 LWWVLCVCSMSVLRAY--PNASPLLGSSWGGLI---HLVYATARN--YHLQIHNGHV 61
DB 13 LWSVYLAGL--LGAQCQHPIDSSPL--QFGQVQRRLVYTDQDTFAHLEINEDGTV 69
QY 62 DGAPHQITVYSLMIRSEDAAGFVITGVMSRRYLCDPFRNIPGSHYFDPENCRFQHOT 121
DB 70 GGAADQSPESILQKALKPVIQILGVKTSRPLCQRPDGLYGSILHFPACSFRELL 129
QY 122 NGDVIDVHSPQYHFLVSL-----GKRAFLPGMNP---PYSQFLSRNEI 164
DB 130 DGVNVYQSEAHGLPLHLPGKNSPHRDPAPRPFLLPLGLPALBEP----- 178
QY 165 PLHFNTPIPRHTRSAEDSERDPPLNVLKPRAPMAPAS 205

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Db 179 ---GILAPOP-----PDVGSDDLPMWGVSGRSPSYAS 209

RESULT 5

PGF3_HUMAN STANDARD; PRT; 216 AA.

AC 095750;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-19 precursor (FGF-19).
GN FGF19.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99132028; PubMed=9931477;
RA Nishimura T., Usumomiyama Y., Hoshikawa M., Ohuchi H., Itoh N.;
RT "Structure and expression of a novel human FGF, FGF-19, expressed in the fetal brain."
RL Biochim. Biophys. Acta 1444:148-151(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Xie M.-H., Holcomb I., Deuel B., Dowd P., Huang A., Vagts A.,
RA Foster J., Bush J., Gu Q., Liang J., Hillan K., Goddard A.,
RA Gurney A.L.;
RT "FGF-19, a novel fibroblast growth factor with unique specificity for FGFR4."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY BE INVOLVED IN BRAIN DEVELOPMENT DURING EMBRYOGENESIS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN FETAL BRAIN.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

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CC -----
DR EMBL; AB018122; BAA75500.1; -
DR EMBL; AF110400; AAD45973.1; -
DR EMBL; BC017664; AAH17664.1; -
DR HSSP; P09038; IBFG.
DR Genew; HGNC:3675; FGF19.
DR MIM; 603891; -
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF.1.
DR PRINTS; PR00262; ILHBGF.
DR PRODOM; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF.1.
DR PROSITE; PS00247; HBGF_FGF.1.
DR Growth factor; Signal.
FT SIGNAL 1 22
FT CHAIN 23 216 POTENTIAL.
SQ SEQUENCE 216 AA; 24002 MW; EDBCBQ9C220F9832 CRC64;

Query Match 15.2%; Score 207; DB 1; Length 216;
Best Local Similarity 28.8%; Pred. No. 9.9e-12;
Matches 67; Conservative 31; Mismatches 91; Indels 44; Gaps 6;

Qy 6 LRLWCAICVCSMSVLAAYENASPLLGSSWGW---LIHLYTATAR--NSYHLOIHKNGH 60
Db 8 VHWIILAGLWLAAGRPPLAFSDAGPHVHYGWDPIRLRLHLYTSGPHGSSCFRLRADGV 67
Qy 61 VDGAHQTIYSALMIRSDAGFVITGVMSRRYLQMPFRGNI FGSHPDPNCRFOHTL 120
Db 68 VDCARGOSAHSLLEIKVAALRTVAIKGVHSVRLQMGADGMOGLQYSEDCAFEEIR 127
Qy 121 ENGIDVHSPQHYHLVSLGRKRAFLFGAMP PPSQFSRNEIPLIHNTPIPRHTRS 180
Db 128 PDGVNVYRSEKGRPLVSLSSAKQ-----RQLYKNKGFPLSHFLMLP----- 170
Qy 181 AEDSERPLNVLKPRAMP-APASCSQELPSAEDNSPM---ASDPIGVYRG 229
Db 171 -----MDEPEEDIRGHLSDMFSPLETSDMDEPLVTG 205

RESULT 6

FGF3_MOUSE STANDARD; PRT; 245 AA.

AC P05524;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3) (FGF-3) (HBGF-3).
GN FGF3 OR FGF-3 OR INT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86247582; PubMed=3013624;
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topography and protein coding potential of mouse int-2: a putative oncogene activated by mouse mammary tumour virus."
RL EMBO J. 5:919-924(1986).
RN [2]
RP SEQUENCE OF 1-73 FROM N.A.
RX MEDLINE=88296404; PubMed=2841106;
RA Smith R., Peters G., Dickson C.;
RT "Multiple RNAs expressed from the int-2 gene in mouse embryonal carcinoma cell lines encode a protein with homology to fibroblast growth factors."
RL EMBO J. 7:1013-1022(1988).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=91193291; PubMed=1964688;
RA Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllian D.,
RA Walther W., Fuller-Pace F., Klefer P., Peters G.;
RT "Characterization of int-2: a member of the fibroblast growth factor family."
RL J. Cell Sci. Suppl. 13:87-96(1990).

CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -1- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

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CC -----
DR EMBL; Y00848; CAA68767.1; -
DR PIR; A23930; TWST2.
DR HSSP; P09038; IBFG.
DR MGD; MGI:95517; FGF3.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.

DR PFAM: PF00167; FGF, 1.
 DR PRINTS: PR00262; IL1HBGF.
 DR PRODOM: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF, 1.
 DR PROSITE: PS00247; HBGF_FGF, 1.
 DR PROTO-ONCOGENE; Growth factor; Mitogen; Signal; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 245 INT-2 PROTO-ONCOGENE PROTEIN.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC...)
 FT SEQUENCE 245 AA; 27214 MW; 70D94F6A7837C79 CRC64;
 SQ
 Query Match 13.4%; Score 182.5; DB 1; Length 245;
 Best Local Similarity 29.4%; Pred. No. 1.9e-09;
 Matches 63; Conservative 26; Mismatches 88; Indels 37; Gaps 8;
 QY 42 LYTATANSYHLQHKNGVDGAPHQITYSALMIRSEDAFVITGVMSRRYLQMDFFGN 101
 DB 48 LYCAT---KYHLQLHPSSGRVNGSLNSAYSLILEITAVEGVVAIKGLPSGRYLAANKGR 104
 QY 102 IFGSHYPPENCRRHQHLENGVDYHSPQYHFLVSLGRAKAFILGNMP----- 152
 DB 105 LYASDHVAAE-CEFYERLHELGNTYASRLYRTGSSGPACRO--PGAQRPVYVSVNGKG 161
 QY 153 -PYGFLSRNEIPLIHNTPIPR-----RHTSAEDDSERDPLNLKPRARMTAPA 204
 DB 162 RPRGFKTRTKQKSLF---LPRVLGHKHHEMVRLLQSSQPRAPGEGSQPROR----- 211
 QY 205 SCSQELPSAEDNSPMASDPLGVNRRGVNTAG 238
 DB 212 --RQKQSPGDHGM--ETLSRATPSTQLHTGG 241
 RESULT 7
 FGF3_HUMAN
 ID FGF3_HUMAN STANDARD; PRT; 239 AA.
 AC P11487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
 DE (FGF-3) (HBGF-3).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA MEDLINE=89239468; PubMed=2470007;
 RA Brooke S., Smith R., Casey G., Dickson C., Peters G.;
 RT "Sequence organization of the human int-2 gene and its expression in
 teratocarcinoma cells."
 RL Oncogene 4:429-436(1989).
 CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
 CC
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 CC
 CC EMBL: X14445; CA32615.1; -
 CC PIR: S04742; S04742.
 CC HSSP: P31371; IGB2.
 CC Genew: HGNC:3681; FGF3.
 CC MIM: 164950; -
 CC InterPro: IPR002209; HB/F_growthfact.
 CC InterPro: IPR002348; IL1_HBGF.
 DR PFAM: PF00167; FGF, 1.

DR PRINTS: PR00262; IL1HBGF.
 DR PRODOM: PD000831; HB/F_growthfact; 1.
 DR SMART: SM00442; FGF, 1.
 DR PROSITE: PS00247; HBGF_FGF, 1.
 DR PROTO-ONCOGENE; Growth factor; Mitogen; Signal; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 239 INT-2 PROTO-ONCOGENE PROTEIN.
 FT CARBOHYD 65 65 N-LINKED (GLCNAC...)
 FT SEQUENCE 239 AA; 26886 MW; 8DBEFL7DB2E3C63 CRC64;
 SQ
 Query Match 13.3%; Score 180.5; DB 1; Length 239;
 Best Local Similarity 31.0%; Pred. No. 2.8e-09;
 Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;
 QY 42 LYTATANSYHLQHKNGVDGAPHQITYSALMIRSEDAFVITGVMSRRYLQMDFFGN 101
 DB 48 LYCAT---KYHLQLHPSSGRVNGSLNSAYSLILEITAVEGVVAIKGLPSGRYLAANKGR 104
 QY 102 IFGSHYPPENCRRHQHLENGVDYHSPQYHFLVSL-----GRAKAFILGNMP--P 153
 DB 105 LYASDHVAAE-CEFYERLHELGNTYASRLYRTVSTPGAROPSAEHLWVSVNGKGRP 163
 QY 154 YSOFLSRNEIPLIHNTPIPRH---TRSAEDDSERDPLNLKPRAR 198
 DB 164 RRGFKTRTKQKSLFLEPRVLDRHHEMVRLLQSSQPRAPGEGSQPROR----- 211
 RESULT 8
 FGF3_XENLA
 ID FGF3_XENLA STANDARD; PRT; 237 AA.
 AC P36386;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3) (INT-2).
 DE FGF3.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]
 RN SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RP MEDLINE=94038898; PubMed=8223431;
 RA Klefer P., Mathieu M., Close J.M., Peters G., Dickson C.;
 RT "FGF3 from Xenopus laevis."
 RL EMBO J. 12:4159-4168(1993).
 RN [2]
 RP SEQUENCE OF 39-137 FROM N.A.
 RC TISSUE=Neurula;
 RA MEDLINE=93048831; PubMed=1425349.
 RA Tamahill D., Isaacs H.V., Close M.J., Peters G., Slack J.M.W.;
 RT "Developmental expression of the Xenopus int-2 (FGF-3) gene:
 RT activation by mesodermal and neural induction."
 RL Development 115:695-702(1992).
 CC -1- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC
 CC EMBL: Z25539; CA480987.1; -
 CC PIR: X65237; CA46341.1; -
 CC HSSP: S39582; S39582.
 CC PIR: S25713; S25713.
 CC HSSP: P31371; IGB2.
 CC InterPro: IPR002209; HB/F_growthfact.
 CC InterPro: IPR002348; IL1_HBGF.

DR PFAM; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KM Growth factor; Mitogen; signal; Glycoprotein.
 FT SIGNAL 1 21
 FT CHAIN 22 237
 FT CARBOHYD 83 83
 SQ SEQUENCE 237 AA; 26984 MW; EDD31B0893567A2D CRC64;

Query March 13.1%; Score 178.5; DB 1; Length 237;
 Best Local Similarity 32.2%; Pred. No. 4.3e-09;
 Matches 55; Conservative 26; Mismatches 63; Indels 27; Gaps 8;

QY 42 LYTAANSYHLQIHKNQVNDGA-PHOTYTSALMTRSEDAGVVTGVMSRRYLQMDPRG 100
 DB 66 LYCAT---KYLQIHKNQVNDGA-PHOTYTSALMTRSEDAGVVTGVMSRRYLQMDPRG 122
 QY 101 NIFSGHYDPENCRCFOHQLENGVDVHSPDYHPLVS-----LGRAKAPLPGMNP-- 152
 DB 123 RLVASETNPE-CEFEVRIHELGYNTYASRLYRTVPSGAGTRKASAEELMWVSINGKR 181
 QY 153 PYSGPLSRN-----FLIHFN---TPIPRHTSAEDSDERDLNVLKP 195
 DB 182 PRSGFKTRTKSSLPFLPRVLNKHDAVRLPHTNAVRES-----ILKP 226

RESULT 9
 FGF5_RAT STANDARD; PRT; 266 AA.
 AC P48807; Q63402;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5).
 GN FGF5 OR FGF-5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC STRAIN=Mistar;
 RX MEDLINE=96201703; PubMed=8611621;
 RA Hattori Y., Yamasaki M., Itoh N.;
 RT "The rat FGF-5 mRNA variant generated by alternative splicing encodes
 a novel truncated form of FGF-5.";
 RL Biochim. Biophys. Acta 1306:31-33(1996).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 SHORT FORM/FGF-5; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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DR EMBL; D64085; BAA10966.1; -
 DR EMBL; D64086; BAA10967.1; -
 DR HSSP; P09038; 1BFG.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KM Proto-oncogene; Growth factor; Mitogen; signal; Alternative splicing.
 FT SIGNAL 1 17
 FT SIGNAL 1 17

FT CHAIN 18 266
 FT DOMAIN 54 59
 FT CARBOHYD 108 108
 FT VARSPIC 118 121
 FT VARSPLIC 122 266
 SQ SEQUENCE 266 AA; 29264 MW; 95B0AC7C0A200C CRC64;

Query March 13.0%; Score 176.5; DB 1; Length 266;
 Best Local Similarity 28.2%; Pred. No. 7.5e-09;
 Matches 58; Conservative 34; Mismatches 75; Indels 39; Gaps 8;

QY 28 ASPLIGSGWGLI---LYTATANS-----YHLQIHKNQVNDGA-PHOTYTSALM 74
 DB 63 ASP-GSGSGSHSSFPWSPSGRGTSLYCVGIGFHLQIYPDGKXVSGHSAVLSILE 120
 QY 75 IRSRAGVVTGVMSRRYLQMDPRGIFGSHYDPENCRCFOHQLENGVDVHSPDYHPLVS 129
 DB 121 IFAVSQIGVIRGVPNSNFKLMSKKGKILHSAKF-TDCKFRERPOENSNTYASAIHRT 179
 QY 130 -----POYHPLVSLGRAKRAFLPGMNPPEYS-QFLSR--RNEIPLIHNTPIPRHTSA 181
 DB 180 EKTREWVVALNKGKAKAGSGSPRVKPGHVSHTLPKPSQSEFELSTYVPER----- 234
 QY 182 EDSERDPLNVLKPRAPNTAPASCS 207
 DB 235 -----KKPPRWKPKVPLSPSRSPS 255

RESULT 10
 FGF5_MOUSE STANDARD; PRT; 264 AA.
 AC P15656; O88825;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5).
 GN FGF5 OR FGF-5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RC MEDLINE=90201563; PubMed=2318343;
 RX Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;
 RT "Isolation of cDNAs encoding four mouse FGF family members and
 RT characterization of their expression patterns during embryogenesis.";
 RL Dev. Biol. 138:454-463(1990).
 CC [2]
 RP SEQUENCE FROM N.A. (LONG ISOFORM).
 RC STRAIN=C57BL/6;
 RX MEDLINE=91045929; PubMed=1700424;
 RA Haub O., Drucker B., Goldfarb M.;
 RT "Expression of the murine fibroblast growth factor 5 gene in the
 RT adult central nervous system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
 CC [3]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RA Oawa K., Suzuki S., Asada M., Tomooka Y., Li A., Yoneda A., Komi A.,
 RA Imamura T.;
 RT "An alternatively-spliced FGF-5 mRNA is abundant in brain and
 RT translates into a partial agonist/antagonist for FGF-5 neurotrophic
 RT activity.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 SHORT FORM/FGF-5; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC DR EMBL, M30643; AAA96698.1; -.
CC DR EMBL, M37823; AAB02660.1; -.
CC DR EMBL, M37821; AAB02660.1; JOINED.
CC DR EMBL, M37822; AAB02660.1; JOINED.
CC DR EMBL, M37821; AAB02659.1; ALT_SEQ.
CC DR EMBL, AB016516; BAA33737.1; -.
CC DR PIR, A36207; A36207.
CC DR PIR, B37360; B37360.
CC DR HSSP, P09038; IBRG.
CC DR MGD; MGI:95519; Fgf5.
CC DR InterPro; IPR002209; HB/F_growthfact.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF, 1.
CC DR PRINTS; PR00262; ILHBGF.
CC DR ProDom; PD000831; HB/F_growthfact; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF, 1.
CC KM Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
CC FT SIGNAL 1 17
CC FT CHAIN 18 264
CC FT DOMAIN 53 59
CC FT CAROHD 108 108
CC FT VARSPLIC 118 121
CC FT VARSPLIC 112 264
CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
Query Match 12.6%; Score 171; DB 1; Length 264;
Best Local Similarity 27.9%; Pred. No. 2.3e-08;
Matches 57; Conservative 35; Mismatches 72; Indels 40; Gaps 9;
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CC DR EMBL, M30643; AAA96698.1; -.
CC DR EMBL, M37823; AAB02660.1; -.
CC DR EMBL, M37821; AAB02660.1; JOINED.
CC DR EMBL, M37822; AAB02660.1; JOINED.
CC DR EMBL, M37821; AAB02659.1; ALT_SEQ.
CC DR EMBL, AB016516; BAA33737.1; -.
CC DR PIR, A36207; A36207.
CC DR PIR, B37360; B37360.
CC DR HSSP, P09038; IBRG.
CC DR MGD; MGI:95519; Fgf5.
CC DR InterPro; IPR002209; HB/F_growthfact.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF, 1.
CC DR PRINTS; PR00262; ILHBGF.
CC DR ProDom; PD000831; HB/F_growthfact; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF, 1.
CC KM Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
CC FT SIGNAL 1 17
CC FT CHAIN 18 264
CC FT DOMAIN 53 59
CC FT CAROHD 108 108
CC FT VARSPLIC 118 121
CC FT VARSPLIC 112 264
CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
Query Match 12.6%; Score 171; DB 1; Length 264;
Best Local Similarity 27.9%; Pred. No. 2.3e-08;
Matches 57; Conservative 35; Mismatches 72; Indels 40; Gaps 9;
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CC DR EMBL, M30643; AAA96698.1; -.
CC DR EMBL, M37823; AAB02660.1; -.
CC DR EMBL, M37821; AAB02660.1; JOINED.
CC DR EMBL, M37822; AAB02660.1; JOINED.
CC DR EMBL, M37821; AAB02659.1; ALT_SEQ.
CC DR EMBL, AB016516; BAA33737.1; -.
CC DR PIR, A36207; A36207.
CC DR PIR, B37360; B37360.
CC DR HSSP, P09038; IBRG.
CC DR MGD; MGI:95519; Fgf5.
CC DR InterPro; IPR002209; HB/F_growthfact.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF, 1.
CC DR PRINTS; PR00262; ILHBGF.
CC DR ProDom; PD000831; HB/F_growthfact; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF, 1.
CC KM Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
CC FT SIGNAL 1 17
CC FT CHAIN 18 264
CC FT DOMAIN 53 59
CC FT CAROHD 108 108
CC FT VARSPLIC 118 121
CC FT VARSPLIC 112 264
CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
Query Match 12.6%; Score 171; DB 1; Length 264;
Best Local Similarity 27.9%; Pred. No. 2.3e-08;
Matches 57; Conservative 35; Mismatches 72; Indels 40; Gaps 9;
-----
CC DR EMBL, M30643; AAA96698.1; -.
CC DR EMBL, M37823; AAB02660.1; -.
CC DR EMBL, M37821; AAB02660.1; JOINED.
CC DR EMBL, M37822; AAB02660.1; JOINED.
CC DR EMBL, M37821; AAB02659.1; ALT_SEQ.
CC DR EMBL, AB016516; BAA33737.1; -.
CC DR PIR, A36207; A36207.
CC DR PIR, B37360; B37360.
CC DR HSSP, P09038; IBRG.
CC DR MGD; MGI:95519; Fgf5.
CC DR InterPro; IPR002209; HB/F_growthfact.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF, 1.
CC DR PRINTS; PR00262; ILHBGF.
CC DR ProDom; PD000831; HB/F_growthfact; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF, 1.
CC KM Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
CC FT SIGNAL 1 17
CC FT CHAIN 18 264
CC FT DOMAIN 53 59
CC FT CAROHD 108 108
CC FT VARSPLIC 118 121
CC FT VARSPLIC 112 264
CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
Query Match 12.6%; Score 171; DB 1; Length 264;
Best Local Similarity 27.9%; Pred. No. 2.3e-08;
Matches 57; Conservative 35; Mismatches 72; Indels 40; Gaps 9;
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CC DR EMBL, M30643; AAA96698.1; -.
CC DR EMBL, M37823; AAB02660.1; -.
CC DR EMBL, M37821; AAB02660.1; JOINED.
CC DR EMBL, M37822; AAB02660.1; JOINED.
CC DR EMBL, M37821; AAB02659.1; ALT_SEQ.
CC DR EMBL, AB016516; BAA33737.1; -.
CC DR PIR, A36207; A36207.
CC DR PIR, B37360; B37360.
CC DR HSSP, P09038; IBRG.
CC DR MGD; MGI:95519; Fgf5.
CC DR InterPro; IPR002209; HB/F_growthfact.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF, 1.
CC DR PRINTS; PR00262; ILHBGF.
CC DR ProDom; PD000831; HB/F_growthfact; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF, 1.
CC KM Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
CC FT SIGNAL 1 17
CC FT CHAIN 18 264
CC FT DOMAIN 53 59
CC FT CAROHD 108 108
CC FT VARSPLIC 118 121
CC FT VARSPLIC 112 264
CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
Query Match 12.6%; Score 171; DB 1; Length 264;
Best Local Similarity 27.9%; Pred. No. 2.3e-08;
Matches 57; Conservative 35; Mismatches 72; Indels 40; Gaps 9;
-----
CC DR EMBL, M30643; AAA96698.1; -.
CC DR EMBL, M37823; AAB02660.1; -.
CC DR EMBL, M37821; AAB02660.1; JOINED.
CC DR EMBL, M37822; AAB02660.1; JOINED.
CC DR EMBL, M37821; AAB02659.1; ALT_SEQ.
CC DR EMBL, AB016516; BAA33737.1; -.
CC DR PIR, A36207; A36207.
CC DR PIR, B37360; B37360.
CC DR HSSP, P09038; IBRG.
CC DR MGD; MGI:95519; Fgf5.
CC DR InterPro; IPR002209; HB/F_growthfact.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF, 1.
CC DR PRINTS; PR00262; ILHBGF.
CC DR ProDom; PD000831; HB/F_growthfact; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF, 1.
CC KM Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
CC FT SIGNAL 1 17
CC FT CHAIN 18 264
CC FT DOMAIN 53 59
CC FT CAROHD 108 108
CC FT VARSPLIC 118 121
CC FT VARSPLIC 112 264
CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
Query Match 12.6%; Score 171; DB 1; Length 264;
Best Local Similarity 27.9%; Pred. No. 2.3e-08;
Matches 57; Conservative 35; Mismatches 72; Indels 40; Gaps 9;
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CC DR EMBL, M30643; AAA96698.1; -.
CC DR EMBL, M37823; AAB02660.1; -.
CC DR EMBL, M37821; AAB02660.1; JOINED.
CC DR EMBL, M37822; AAB02660.1; JOINED.
CC DR EMBL, M37821; AAB02659.1; ALT_SEQ.
CC DR EMBL, AB016516; BAA33737.1; -.
CC DR PIR, A36207; A36207.
CC DR PIR, B37360; B37360.
CC DR HSSP, P09038; IBRG.
CC DR MGD; MGI:95519; Fgf5.
CC DR InterPro; IPR002209; HB/F_growthfact.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF, 1.
CC DR PRINTS; PR00262; ILHBGF.
CC DR ProDom; PD000831; HB/F_growthfact; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF, 1.
CC KM Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
CC FT SIGNAL 1 17
CC FT CHAIN 18 264
CC FT DOMAIN 53 59
CC FT CAROHD 108 108
CC FT VARSPLIC 118 121
CC FT VARSPLIC 112 264
CC SQ SEQUENCE 264 AA; 29103 MW; F6A9C8153EE923D1 CRC64;
Query Match 12.6%; Score 171; DB 1; Length 264;
Best Local Similarity 27.9%; Pred. No. 2.3e-08;
Matches 57; Conservative 35; Mismatches
```

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RA MEDLINE=89069642; PubMed=3211147;
RX Zhan X., Bates B., Hu X., Goldfarb M.;
RT "The human FGF-5 oncogene encodes a novel protein related to
RL fibroblast growth factors.";
RN Mol. Cell. Biol. 8:3487-3495(1988).
RN [3]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RA Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A., Yoneda A., Komai A.,
RA Imamura T.;
RT "An alternatively-spliced FGF-5 mRNA is abundant in brain and
RT translates into a partial agonist/antagonist for FGF-5 neurotrophic
RT activity";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC TISSUE=Umbilical artery;
RX MEDLINE=20379035; PubMed=10823842;
RA de Vries C.W.J.M., van Achterberg T.A.E., Horrevoets A.J.G.,
RA ten Cate J.W., Pannekoek H.;
RT "Differential display identification of 40 genes with altered
RT expression in activated human smooth muscle cells. Local expression
RT in atherosclerotic lesions of smags, smooth muscle
RT activation-specific genes.";
RL J. Biol. Chem. 275:23939-23947(2000).
CC -1- FUNCTION: THIS ONCGENE IS EXPRESSED IN NEONATAL BRAIN. FGF-5 CAN
CC TRANSFORM NIH 3T3 CELLS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM/FGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC or send an email to licens@isb-sib.ch).
CC -----
CC EMBL; M37825; AAB06463.1; .-
DR EMBL; M23536; AAB60699.1; .-
DR EMBL; M23534; AAB60699.1; JOINED.
DR EMBL; M23535; AAB60699.1; JOINED.
DR EMBL; M23534; AAB60699.1; ALT_SEQ.
DR EMBL; AB016517; BA033738.1; .-
DR EMBL; AF171928; AAFF89742.1; .-
DR PIR; A31194; TVHUF5.
DR HSSP; P09038; IBFG.
DR Genew; HGNC:3683; FGFS.
DR MIM; 165190; .-
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IHL_HBGF.
DR Pfam; PF00167; FGF_1.
DR PRINTS; PR00262; ILHBGF.
DR Prodom; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF_1.
DR PROSITE; PS00247; HBGF_FGF_1.
DR PicO-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
FW SIGNAL 1 17 POTENTIAL.
FT CHAIN 49 52 FIBROBLAST GROWTH FACTOR-5.
FT DOMAIN 18 55 POLY-SER.
FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
FT VASPLIC 120 123 VLFI -> OVHR (IN SHORT ISOFORM).
FT VASPLIC 124 268 MISSING (IN SHORT ISOFORM).
FT CONFLICT 42 42 R -> I (IN REF. 1).
FT CONFLICT 83 86 PSGR -> LGA (IN REF. 2).
SO SEQUENCE 268 AA; 29526 MW; 08F4268B6781B9D CRC64;

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Db 52 SAMSSSSSSSSPPAS--LGSOGSSGLEGSSFGWSPGSRRTGSLYCVGIGFHLQIYDPGKV 109
Qy 62 DGAPHQITYSALMIRSEDAFVITGWSRRYLQMDFGNIGSHYFDPENCFOHOTLE 121
Db 110 NGSHEANLWLVLEIFAVSQGIVGIGVSNKFLAMSKKCKLHAKAF--TDCKFERROE 168
Qy 122 NGYVYTHS-----POYHFLVSLGRAKRAFLPGMNPPTS-QPLSR--RNEIPLIH 168
Db 169 NSYNTYASAIHRTKXTGKREWYVALNKRGKAKGCSPRVQPIIHTHPLPRFQSSQPELS 228
Qy 169 ENTPIPRR 176
Db 229 FTVTPEK 236

RESULT 12
FGF3_CHICK
ID_FGF3_CHICK STANDARD; PRT; 220 AA.
AC P48801;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3).
GN FGF3 OR FGF-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Teleostei; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rhode Island red; TISSUE=Embryo;
RX MEDLINE=95309122; PubMed=7789270;
RA Mahmood R., Kiefer P., Guthrie S., Dickson C., Mason I.;
RT "Multiple roles for FGF-3 during cranial neural development in the
RT chicken.";
RL Development 121:1399-1410(1995).
CC -1- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC -----
DR EMBL; Z47555; CAAB7635.1; -.
DR HSSP; P31371; 1682.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF, 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF, 1.
DR PROSITE; PS00247; HBGF_FGF, 1.
DR Growth factor; Mitogen; Signal; Glycoprotein.
FT CHAIN 1 19 POTENTIAL.
FT SIGNAL 20 220 FIBROBLAST GROWTH FACTOR-3.
FT CARBOHYD 66 66 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 220 AA; 25050 MW; B15DA1D1E551C5D5 CRC64;

Query Match 12.3%; Score 167; DB 1; Length 220;
Best Local Similarity 33.3%; Pred. No. 4.3e-08;
Matches 49; Conservative 18; Mismatches 70; Indels 10; Gaps 4;

Qy 6 LRLW--VQALCSVCSMSVLRAPNAPSPLGSSWGGLIHLVTATAR-----NSYHLQIHK 57
Db 2 LVIMLLALILPEPRVVPATASPRAPRDAGRGVYEHLGAPRRARKYCATKYLQIHP 61
Qy 58 NGHVDGA-PHQITYSALMIRSEDAFVITGWSRRYLQMDFGNIGSHYFDPENCFO 116

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Db 62 GCKINGTLEKNSVPSILLETITVDVGIVAIKGLFSGRYLANKRGRLVASENMYTE-CEPV 120
Qy 117 HOTLENGVDVYHSPQYHFLVSLGRAKR 143
Db 121 ERIHELGINTYASRLRYTPSGASTKR 147

RESULT 13
FGF3_BRARE
ID_FGF3_BRARE STANDARD; PRT; 256 AA.
AC P48802;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3).
GN FGF3 OR FGF-3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96204005; PubMed=8622866;
RA Kiefer P., Strahle U., Mason I., Dickson C.;
RT "Secretion and mitogenic activity of zebrafish FGF3 reveal
RT intermediate properties relative to mouse and Xenopus homologues.";
RL Oncogene 12:1503-1511(1996).
CC -1- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC -----
DR EMBL; Z48714; CAAB8596.1; -.
DR HSSP; P09038; 1BFG.
DR ZFIN; ZDB-GENE-980526-178; fgf3.
DR InterPro; IPR002209; HB/F_growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF, 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; HB/F_growthfact; 1.
DR SMART; SM00442; FGF, 1.
DR PROSITE; PS00247; HBGF_FGF, 1.
DR Growth factor; Mitogen; Signal; Glycoprotein.
FT CHAIN 1 18 POTENTIAL.
FT SIGNAL 19 256 FIBROBLAST GROWTH FACTOR-3.
SQ SEQUENCE 256 AA; 28923 MW; CEBAC7A170BDBC CRC64;

Query Match 11.7%; Score 159.5; DB 1; Length 256;
Best Local Similarity 37.2%; Pred. No. 2.5e-07;
Matches 42; Conservative 13; Mismatches 39; Indels 19; Gaps 5;

Qy 42 LYTATANSYHLOIHKXGNDGA-PHQITYSALMIRSEDAFVITGWSRRYLQMDFG 100
Db 66 LYCAT--KYLQIHPKNGKIDSLBNPNLSILITITVDVGVAIKGLFSGRYLANMEKG 122
Qy 101 NIFGSHVEDPENCFOHOTLENGVDVYHSPQYHFLVSLGRAKRAFLPGMNP 153
Db 123 RLVASEVYNR-CEFLRIHILGINTYAS-RHAAIT-----QPP 160

RESULT 14
FGFB_XENLA
ID_FGFB_XENLA STANDARD; PRT; 192 AA.
AC P48805;
DT 01-FEB-1996 (Rel. 33, Created)

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibroblast growth factor-4-II precursor (FGF-4-II) (HBGF-4-II)
 DE Embryonic fibroblast growth factor II) (XERGF-II).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 NCBI_TaxID=8335;
 RX MEDLINE=92315916; PubMed=1618138;
 RA Isaacs H.V., Tamahill D., Slack J.M.W.;
 RT "Expression of a novel FGF in the Xenopus embryo. A new candidate
 RT inducing factor for mesoderm formation and anteroposterior
 RT specification.";
 RL Development 114:711-720(1992).
 CC -1- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE
 CC ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE
 CC FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC -----
 DR EMBL; X62594; CAA44480.1; -
 DR HSSP; P31371; 1682.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 DR Growth factor; Mitogen; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 192
 FT SEQUENCE 192 AA; 21903 MW; 2B01B0B8824E3B3 CRC64;
 SQ
 Query Match 11.4%; Score 155; DB 1; Length 192;
 Best Local Similarity 31.9%; Pred. No. 4.4e-07;
 Matches 30; Conservative 25; Mismatches 37; Indels 2; Gaps 2;
 QY 51 YHLOIHKNQHVDAFHQTYALMIRSEDAFGVITGVMSRRYLCMDPRGNIFGSHYDP 110
 DB 80 FHIOVLPGRLNGMSENRYSLEISPEVGVVSLYGVKSGMFVAMNAKGLYGSRYFN- 138
 QY 111 ENCRFOHOTLENGDVVHSPOY-HFLVSLGRAR 143
 DB 139 BECKFKETLLPNNVAYESRKYPGMYIALGKGR 172
 RESULT 15
 ID FGFA_XENLA STANDARD; PRT; 187 AA.
 AC P48805;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibroblast growth factor-4-I precursor (FGF-4-I) (HBGF-4-I) (Embryonic
 DE fibroblast growth factor I) (XERGF-I).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodinae; Xenopus.
 NCBI_TaxID=8335;
 RX MEDLINE=92315916; PubMed=1618138;
 RA Isaacs H.V., Tamahill D., Slack J.M.W.;
 RT "Expression of a novel FGF in the Xenopus embryo. A new candidate
 RT inducing factor for mesoderm formation and anteroposterior
 RT specification.";
 RL Development 114:711-720(1992).
 CC -1- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE
 CC ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE
 CC FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC -----
 DR EMBL; X62593; CAA44479.1; -
 DR HSSP; P31371; 1682.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 DR Growth factor; Mitogen; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 187
 FT SEQUENCE 187 AA; 21223 MW; AA63D658582AD1BD CRC64;
 SQ
 Query Match 11.1%; Score 151; DB 1; Length 187;
 Best Local Similarity 31.9%; Pred. No. 9.8e-07;
 Matches 30; Conservative 24; Mismatches 38; Indels 2; Gaps 2;
 QY 51 YHLOIHKNQHVDAFHQTYALMIRSEDAFGVITGVMSRRYLCMDPRGNIFGSHYDP 110
 DB 75 FHIOVLPGRLNGMSENRYSLEISPEVGVVSLYGVKSGMFVAMNAKGLYGSRYFN- 133
 QY 111 ENCRFOHOTLENGDVVHSPOY-HFLVSLGRAR 143
 DB 134 BECKFKETLLPNNVAYESRKYPGMYIALGKGR 167

RP SEQUENCE FROM N.A.
 RX MEDLINE=92315916; PubMed=1618138;
 RA Isaacs H.V., Tamahill D., Slack J.M.W.;
 RT "Expression of a novel FGF in the Xenopus embryo. A new candidate
 RT inducing factor for mesoderm formation and anteroposterior
 RT specification.";
 RL Development 114:711-720(1992).
 CC -1- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE
 CC ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE
 CC FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC -----
 DR EMBL; X62593; CAA44479.1; -
 DR HSSP; P31371; 1682.
 DR InterPro; IPR002209; HB/F_growthfact.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HB/F_growthfact; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 DR Growth factor; Mitogen; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 187
 FT SEQUENCE 187 AA; 21223 MW; AA63D658582AD1BD CRC64;
 SQ
 Query Match 11.1%; Score 151; DB 1; Length 187;
 Best Local Similarity 31.9%; Pred. No. 9.8e-07;
 Matches 30; Conservative 24; Mismatches 38; Indels 2; Gaps 2;
 QY 51 YHLOIHKNQHVDAFHQTYALMIRSEDAFGVITGVMSRRYLCMDPRGNIFGSHYDP 110
 DB 75 FHIOVLPGRLNGMSENRYSLEISPEVGVVSLYGVKSGMFVAMNAKGLYGSRYFN- 133
 QY 111 ENCRFOHOTLENGDVVHSPOY-HFLVSLGRAR 143
 DB 134 BECKFKETLLPNNVAYESRKYPGMYIALGKGR 167

Search completed: May 23, 2003, 07:43:46
 Job time : 26 secs

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OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:52 ; Search time 20 Seconds

(without alignments)
1206.487 Million cell updates/sec

Title: US-09-901-938-2

Perfect score: 1360

Sequence: 1 MLAGRLRLMWCAALCSVCSSMS.....VNTHAGTGPEGRCPFAKFI 251

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	961	70.7	251	2	JC7513 fibroblast growth
2	182.5	13.4	245	1	TCVMS72 transforming prote
3	180.5	13.3	239	1	SO4742 fibroblast growth
4	178.5	13.1	237	1	SG9582 transforming prote
5	176.5	13.0	266	2	SG8144 fibroblast growth
6	171	12.6	264	2	A36207 fibroblast growth
7	169	12.4	267	1	TVHUP5 fibroblast growth
8	167	12.3	220	2	I50588 fibroblast growth
9	159.5	11.7	256	2	JC4627 fibroblast growth
10	155	11.4	192	2	SG4407 embryonic fibrobla
11	151	11.1	187	2	SG3595 embryonic fibrobla
12	146.5	10.8	194	2	I50710 fibroblast growth
13	141.5	10.4	208	2	SG2102 fibroblast growth
14	138.5	10.2	208	2	SG14192 fibroblast growth
15	138	10.1	206	2	JC4268 fibroblast growth
16	132.5	9.7	211	2	JC7353 fibroblast growth
17	132	9.7	207	2	JC5940 fibroblast growth
18	131.5	9.7	206	1	TVHUS8 fibroblast growth
19	131	9.6	202	1	TVMSHS fibroblast growth
20	130.5	9.6	212	2	JC7511 fibroblast growth
21	129	9.5	207	2	JC5941 fibroblast growth
22	128	9.4	194	2	SG2049 fibroblast growth
23	128	9.4	194	2	I48610 keratinocyte growt
24	127	9.3	168	2	UG0184 fibroblast growth
25	127	9.3	194	2	SG49501 keratinocyte growt
26	126	9.3	194	1	A36301 fibroblast growth
27	121.5	8.9	208	2	JC7082 fibroblast somatoc
28	118	8.7	208	2	SG6486 fibroblast growth
29	118	8.7	208	2	A48137 fibroblast growth

30	117	8.6	154	2	A31674 basic fibroblast g
31	116.5	8.6	154	2	C37360 basic fibroblast g
32	116.5	8.6	164	2	SG1622 basic fibroblast g
33	115.5	8.5	137	2	I46711 fibroblast growth
34	115.5	8.5	146	1	SG0185 basic fibroblast g
35	115.5	8.5	157	1	GKBO8 basic fibroblast g
36	115.5	8.5	210	2	A32398 basic fibroblast g
37	107.5	7.9	155	2	SG4147 basic fibroblast g
38	107.5	7.9	155	2	D37360 acidic fibroblast
39	106.5	7.8	155	2	A60130 acidic fibroblast
40	105.5	7.8	155	1	A60721 acidic fibroblast
41	103	7.6	189	2	A48834 basic fibroblast
42	101	7.4	155	1	GKBOA basic fibroblast
43	100	7.4	215	2	G02092 fibroblast growth
44	100	7.4	215	2	A46245 fibroblast growth
45	99.5	7.3	155	2	JW0055 acidic fibloblast

ALIGNMENTS

RESULT 1
JC7513
fibroblast growth factor-23 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7513
R:Yamashita, T.; Yoshida, M.; Itob, N.
Biochem. Biophys. Res. Commun. 277, 494-498, 2000
A:Title: Identification of a novel fibroblast growth factor, FGF-23, preferentially exp
A:Reference number: JC7513; PMID:20490027; PMID:11032749
A:Contents: Embryo
A:Accession: JC7513
A:Molecule type: mRNA
A:Residues: 1-251 <YAM>
A:Cross-references: DDB:AB037889
C:Comment: This factor, a secreted protein, acts on proximal cells and plays roles in
C:Genetics:
A:Gene: fgf-23
C:Keywords: nucleus

Query Match 70.7%; Score 961; DB 2; Length 251;
Best Local Similarity 70.5%; Pred. No. 5.4e-80;
Matches 177; Conservative 25; Mismatches 49; Indels 0; Gaps 0;

QY	1	MLGARLRLMWCAALCSVCSSMSVLRAPNAPSPLGSSWGLHLVYATARNSTHLQIKNGH	60
DB	1	MLGTCRLRLVGLCTVCSLCTARAVPDTSPLGSSWGLVTLVYATARTSYHLQIKRDGH	60
QY	61	VDGAPHQITVSALMIRSDAGFVVITGVMSRRYLCPMDPRGNIFGSHYDPENCRPHQTL	120
DB	61	VDGTHQITVSALMIRSDAGFVVITGVMSRRYLCPMDPRGNIFGSHYDPENCRPHQTL	120
QY	121	ENGVDVYHSPOYHPLVLSGRKRAFLPGMNPPEYQSLFRNEIPLIHNPPIPRHRS	180
DB	121	ENGIDVYLSQKHVYHSIGRAKRIIPGCTNPPPSQFLARNEVPLHLFVYVRPRHRS	180
QY	181	AEDSERDPLNLVLRAPAMTPAPASCSQELPSAEDNSPMADPDGVVYVGRVNTHAGGTG	240
DB	181	AEDPERPLNLVLRAPAMTPAPASCSQELPSAEDNSPMADPDGVVYVGRVNTHAGGTG	240
QY	241	PEGCRPFPAKFI 251	
DB	241	ADRCRPFPRFV 251	

RESULT 2
TCVMS72
transforming protein (int-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C:Accession: A23930; S08157
R:Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.

EMBO J. 5, 919-924, 1986
 A>Title: Sequence, topography and protein coding potential of mouse int-2: a putative on
 A/Reference number: A23930; MUID:86247582; PMID:5013624
 A/Accession: A23930
 A/Molecule type: DNA; mRNA
 A/Residues: 1-245 <MOO>
 A/Cross-references: GB:Y00848; GB:M26284; GB:X68450; NID:952716; PIDN:CAA68767.1; PID:95
 R:Acland, P.; Dixon, M.; Peters, G.; Dickson, C.
 Nature 343, 663-665, 1990
 A>Title: Subcellular fate of the int-2 oncoprotein is determined by choice of initiation
 A/Reference number: S08157; MUID:90158795; PMID:2406607
 A/Accession: S08157
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: HSRAGLARGVLPAPRLRTRAGAAAAAGRDAGW, 3-17 <ACL>
 A/Genetics:
 A/Gene: int-2
 A/Map position: 7
 A/Introns: 74/1; 108/3
 C/Superfamily: fibroblast growth factor
 C/Keywords: growth factor; transforming protein

Query Match 13.4%; Score 182.5; DB 1; Length 245;
 Best Local Similarity 29.4%; Pred. No. 4.2e-09;
 Matches 63; Conservative 26; Mismatches 88; Indels 37; Gaps 8;

QY 42 LYTATANSYHLOIHKNGHVDGAPHTTYSALMIRSEDAFVVTGVMSRRYLCMPFRGN 101
 DB 48 LYCAT---KTHLQHPSSGRVNGSLNSAYSLILEITAVEGVIAVIGLPSGRILANNKGR 104
 QY 102 IFGSHYDPENCRFQHQTLNGVDYHSPQYHFLVSLGRAKRAFLPGMNP----- 152
 DB 105 LVASDHVNAE-CEFERVHELGINTYASRLYRTGSSGCAQRO--PGAQRPVYVSVNGK 161
 QY 153 -PYSQFLSRNEIPLIHNTPIPR-----RHTSAEDSDERDPLNVLKPRARTRAPA 204
 DB 162 RPRGFTRRQKSSLP-----LPRVLGHKDHENVALLOSOPRABEGSOPROR----- 211
 QY 205 SCQGLPSAEDNSPMASDPLGVNRGRVNTAGG 238
 DB 212 --RQKQSPGDHGM--ETLSTRATPSTQIHTGG 241

RESULT 3
 S04742
 fibroblast growth factor 3 precursor - human
 N/Alternate names: transforming protein int-2
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 29-Sep-1999
 C/Accession: S04742
 R/Brookes, S.; Smith, R.; Casey, G.; Dickson, C.; Peters, G.
 Oncogene 4, 429-436, 1989
 A>Title: Sequence organization of the human int-2 gene and its expression in teratocarc
 A/Reference number: S04742; MUID:9239468; PMID:2470007
 A/Accession: S04742
 A/Molecule type: DNA
 A/Residues: 1-239 <BRO>
 A/Cross-references: EMBL:X14445; NID:933937; PIDN:CAA22615.1; PID:9312409
 C/Genetics:
 A/Gene: GDB:RGF3, INT2
 A/Cross-references: GDB:120103; OMIM:164950
 A/Map position: 11q13.3-11q13.3
 A/Introns: 74/1; 108/3
 C/Superfamily: fibroblast growth factor
 C/Keywords: growth factor
 P:1-17/Domain: signal sequence #status predicted <SIG>
 P:18-239/Product: transforming protein (int-2) #status predicted <MAT>

Query Match 13.3%; Score 180.5; DB 1; Length 239;
 Best Local Similarity 31.0%; Pred. No. 6.1e-09;
 Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

QY 42 LYTATANSYHLOIHKNGHVDGAPHTTYSALMIRSEDAFVVTGVMSRRYLCMPFRGN 101

DB 48 LYCAT---KTHLQHPSSGRVNGSLNSAYSLILEITAVEGVIAVIGLPSGRILANNKGR 104
 QY 102 IFGSHYDPENCRFQHQTLNGVDYHSPQYHFLVSL-----GRAKRAFLPGMNP--P 153
 DB 105 LVASDHVNAE-CEFERVHELGINTYASRLYRTVSGTGAARQSAERLWVSVNGKRP 163
 QY 154 YSQFLSRNEIPLIHNTPIPRR---TRSAEDSDERDPLNVLKPRAR 198
 DB 164 RPRGFTRRQKSSLPFLPVLDRHDEWVRQSGLPFRPPGQVQPRRR 211

RESULT 4
 S39582
 transforming protein int-2 - African clawed frog
 N/Alternate names: FGF-3 protein; fibroblast growth factor 3
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: S39582; S25713
 R/Kiefer, P.; Mathieu, M.; Close, M.D.; Peters, G.; Dickson, C.
 EMBO J. 12, 4159-4168, 1993
 A>Title: FGF3 from Xenopus laevis.
 A/Reference number: S39582; MUID:94038898; PMID:8223431
 A/Accession: S39582
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-237 <KIE>
 A/Cross-references: EMBL:Z25539; NID:9396830; PIDN:CAA80987.1; PID:9396831
 R/Tamamilli, D.; Isaacs, H.V.; Close, M.C.; Peters, G.; Slack, J.M.W.
 Development 115, 695-702, 1992
 A>Title: Developmental expression of the Xenopus int-2 (FGF-3) gene: activation by mes
 A/Reference number: S25713; MUID:93048831; PMID:1425349
 A/Accession: S25713
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 39-137 <TAN>
 A/Cross-references: EMBL:X65237; NID:964855; PIDN:CAA46341.1; PID:964856
 C/Superfamily: fibroblast growth factor

Query Match 13.1%; Score 178.5; DB 1; Length 237;
 Best Local Similarity 32.2%; Pred. No. 9.2e-09;
 Matches 55; Conservative 26; Mismatches 63; Indels 27; Gaps 8;

QY 42 LYTATANSYHLOIHKNGHVDGA-PHOTIYSALMIRSEDAFVVTGVMSRRYLCMPFRG 100
 DB 66 LYCAT---KTHLQHPSSGRVNGSLNSAYSLILEITAVEGVIAVIGLPSGRILANNKGR 122
 QY 101 NIFGSHYDPENCRFQHQTLNGVDYHSPQYHFLVSL-----LGRAKRAFLPGMNP-- 152
 DB 123 RLVASSETYNE-CEFERVHELGINTYASRLYRTVSGAGTKKASAEKRLMYVSIKNGR 181
 QY 153 PYSQFLSRNEIPLIHNTPIPRR---TPPRRHTSAEDSDERDPLNVLKPR 195
 DB 182 RPRGFTRRQKSSLPFLPVLDMKMDHVAVRLPHTNAYRRS-----ILKP 226

RESULT 5
 S68144
 fibroblast growth factor 5 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 06-Dec-1996 #sequence, revision 13-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S68144
 R/Hattori, Y.; Yamaoka, M.; Itoh, N.
 Blochim. Biophys. Acta 1306, 31-33, 1996
 A>Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel
 A/Reference number: S68144; MUID:96201703; PMID:8611821
 A/Accession: S68144
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-266 <HAT>
 A/Cross-references: EMBL:D64085; NID:9992952; PIDN:BAAL0966.1; PID:9992953
 C/Superfamily: fibroblast growth factor

Query Match 13.0%; Score 176.5; DB 2; Length 266;
Best Local Similarity 28.2%; Pred. No. 1.6e-08;
Matches 58; Conservative 34; Mismatches 75; Indels 39; Gaps 8;

QY 28 ASPLLGSSWGLIY---LYTATARN-----YHLOIHNKGHVDPAPHOTIYSALM 74
DB 63 ASP--GSGSGSEHSSFWSPSGSRTGSLYCRVIGIFHLQIYPDGKVNSSHEASVLSILE 120
QY 75 IRSEDAGFVITGVMSRRYLQMDFRGNIFGSHYFDPENCRFQHOTLENGYDVYHS----- 129
DB 121 IFVAVSGIVGRGVSNKFLAMSKKGLHASAKF--TDDCKFERFQENSYNTYASAIHRT 179
QY 130 -----POYHFLVSLGRKRAFLPGMNPPEYS-QFLSR--RNEIPLIHNTPIPRHRTSA 181
DB 180 EKTGREWYVALNKRKAKRGCSPRVKPQHVSTHFLPRFQSEQPELSFTVYPER----- 234
QY 182 EDDSERDPLNLKPRARMTAPASCS 207
DB 235 -----KKPPRPWKPKVPLSPSRSPS 255

RESULT 6

A36207
fibroblast growth factor 5 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 17-Mar-2000
C/Accession: A36207; B37360
R/Haub, O.; Drucker, B.; Goldfarb, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 8022-8026, 1990
A/Title: Expression of the murine fibroblast growth factor 5 gene in the adult central
A/Reference number: A36207; MUID:91045929; PMID:1700424.
A/Accession: A36207
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-264 <HAU>
A/Cross-references: GB:M37821; GB:M37822; GB:M37823; NID:G193280; PIDN:AA802660.1; PID:G
R/Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A/Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A/Reference number: A37360; MUID:90201563; PMID:2318343
A/Accession: B37360
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-264 <HEB>
A/Cross-references: GB:M30643; NID:G193294; PIDN:AAA96698.1; PID:G309238
C/Superfamily: fibroblast growth factor

Query Match 12.6%; Score 171; DB 2; Length 264;
Best Local Similarity 27.9%; Pred. No. 5.1e-08;
Matches 57; Conservative 35; Mismatches 72; Indels 40; Gaps 9;

QY 28 ASPLLGSSWGLIY---LYTATARN-----YHLOIHNKGHVDPAPHOTIYSALM 74
DB 63 ASP--GSGSGSEHSSFWSPSGSRTGSLYCRVIGIFHLQIYPDGKVNSSHEASVLSILE 120
QY 75 IRSEDAGFVITGVMSRRYLQMDFRGNIFGSHYFDPENCRFQHOTLENGYDVYHS----- 129
DB 121 IFVAVSGIVGRGVSNKFLAMSKKGLHASAKF--TDDCKFERFQENSYNTYASAIHRT 179
QY 130 -----POYHFLVSLGRKRAFLPGMNPPEYS-QFLSR--RNEIPLIHNTPIPRHRTSA 181
DB 180 EKTGREWYVALNKRKAKRGCSPRVKPQHVSTHFLPRFQSEQPELSFTVYPER----- 232
QY 182 EDDSERDPLNLKPRARMTAPASCS 203
DB 233 --EKKRPVKVPLSPSRSPS 254

RESULT 7

fibroblast growth factor 5 - human
N:Alternate names: transforming protein FGFS
C/Species: Homo sapiens (man)

C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 17-Mar-2000
C/Accession: A31194
R/Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Mol. Cell. Biol. 8, 3487-3495, 1988
A/Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth
A/Reference number: A31194; MUID:89096942; PMID:3211147
A/Accession: A31194
A/Molecule type: mRNA
A/Residues: 1-267 <ZHA>
A/Cross-references: GB:M23536; GB:M21617; NID:G182539; PIDN:AA806699.1; PID:G182542
C/Genetics:
A/Gene: GDB:FGF5
A/Cross-references: GDB:119907; OMIM:165190
A/Map position: 4q21-4q22
C/Superfamily: fibroblast growth factor
C/Keywords: growth factor; transforming protein

Query Match 12.4%; Score 169; DB 1; Length 267;
Best Local Similarity 30.5%; Pred. No. 7.9e-08;
Matches 57; Conservative 27; Mismatches 75; Indels 28; Gaps 7;

QY 15 SVCSWVLRAYVNASPLIGSSWGLI---IHYTATARN-----GYHLOIHNKGHVDP 62
DB 52 SAMSSSSASSSPAS--IGSGSGIEGSSFWSLGARTGSLYCRVIGIFHLQIYPDGKVN 109
QY 63 GAPHOTIYSALMIRSEDAGFVITGVMSRRYLQMDFRGNIFGSHYFDPENCRFQHOTLEN 122
DB 110 GSHEANMLSVLEIFAVSGIVGRGVSNKFLAMSKKGLHASAKF--TDDCKFERFQEN 168
QY 123 GYDVYHS-----POYHFLVSLGRKRAFLPGMNPPEYS-QFLSR--RNEIPLIHNT 169
DB 169 SYNTYASAIHRTKTEKREWYVALNKRKAKRGCSPRVKPQHVSTHFLPRFQSEQPELSF 228
QY 170 NTPIPRR 176
DB 229 TVTYPER 235

RESULT 8

150588
fibroblast growth factor 3 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000
C/Accession: 150588
R/Mahood, R.; Klefer, P.; Guthrie, S.; Dickson, C.; Mason, I.
Development 121, 1399-1410, 1995
A/Title: Multiple roles for FGF-3 during cranial neural development in the chicken.
A/Reference number: 150588; MUID:95309122; PMID:7789270
A/Accession: 150588
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-220 <MAH>
A/Cross-references: EMBL:Z47555; NID:G623215; PIDN:CAA87635.1; PID:G623216
C/Superfamily: fibroblast growth factor

Query Match 12.3%; Score 167; DB 2; Length 220;
Best Local Similarity 33.3%; Pred. No. 9.3e-08;
Matches 49; Conservative 18; Mismatches 70; Indels 10; Gaps 4;

QY 6 LRIM--VCALCSVCSWVLRAYVNASPLIGSSWGLIHYTATARN-----NSYHLOIHK 57
DB 2 LVIMLLALLLPBRVPAATAAPRADAGRGVHGLGAPRRRLKYCTKTHLQIHP 61
QY 58 NGHYDGA-PHOTIYSALMIRSEDAGFVITGVMSRRYLQMDFRGNIFGSHYFDPENCRFQ 116
DB 62 GSKINGTLERKNVPSILEITAVDVGIVAIKGLFSGRYLANKRGRLVASEVYNT-CEFV 120
QY 117 HOTLENGYDVYHSPOYHFLVSLGRKRA 143
DB 121 BRHLEIGNTYASRLYRTVPSGASTKR 147

RESULT 9

JC4627
 fibroblast growth factor 3 - zebra fish
 C/Species: Brachydanio rerio (zebra fish)
 C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999
 C/Accession: JC4627
 R/RefSeq: P.; Strechle, U.; Dickson, C.
 Gene 168, 211-215, 1996
 A/Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript structure and genomic organ
 A/Reference number: JC4627; MUID:96194899; PMID:8654946
 A/Accession: JC4627
 A/Molecule type: mRNA
 A/Residues: 1-256 <KTB>
 A/Cross-references: EMBL:Z48714; NID:9971333; PIDN:CAA88596.1; PID:9971334
 A/Note: Experimental source: embryo
 A/Note: The authors translated the codon TGG for residue 178 as His
 C/Comment: This factor belongs to the fibroblast growth factor family which have the fur
 osten is a cell signalling molecule and plays the roles during the early stages of devel
 C/Genetics:
 A/Gene: Fgf-3
 A/Intons: 93/2; 127/3
 A/Supersfamily: fibroblast growth factor
 C/Keywords: embryo; fibroblast; growth factor

Query Match 11.7%; Score 159.5; DB 2; Length 256;
 Best Local Similarity 37.2%; Pred. No. 5.5e-07;
 Matches 42; Conservative 13; Mismatches 39; Indels 19; Gaps 5;

42 LYATPANSYHLOHKNHVDGA-PHOTYSALMIRSEDAFGVITGVMSRRYLCMDRGNIFGSHYFDP 100
 Db LYCAT--KYLQHPNKIGSLSENNPLSLLETTADVGVAAKGFSGGYLLMNNKNG 122
 66
 101 NIFGSHYFDPENCERFOHTELENGYDVYHSPQYHFLVSLGRAKRAFLPGNNPP 153
 Db RLVAISEVNR-CEFLERIHLEGVYIAS-RHMT-----QPP 160
 123

RESULT 10
 S54407
 embryonic fibroblast growth factor II - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
 C/Accession: S54407
 R/Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.
 Development 114, 711-720, 1992
 A/Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing facto
 A/Reference number: S23595; MUID:92315916; PMID:1618138
 A/Accession: S54407
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-192 <ISA>
 A/Cross-references: EMBL:X62594; NID:9840919; PIDN:CAA44480.1; PID:9840920
 C/Supersfamily: fibroblast growth factor

Query Match 11.4%; Score 155; DB 2; Length 192;
 Best Local Similarity 31.9%; Pred. No. 9.7e-07;
 Matches 30; Conservative 25; Mismatches 37; Indels 2; Gaps 2;

51 YHLOHKNHVDGAPHOTYSALMIRSEDAFGVITGVMSRRYLCMDRGNIFGSHYFDP 110
 Db FHIQVLPGRINGMHNENRYSLEISPEVGVSLYGIKSAFVAMNKKGLYGRYFN- 138
 80
 111 ENCRFOHTELENGYDVYHSPQY-HFLVSLGRAKR 143
 Db
 139 EECKFKETLLPNNYAYESRKYPGMYIALGKNGR 172

RESULT 11
 S23595
 embryonic fibroblast growth factor - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
 C/Accession: S23595
 R/Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.

Development 114, 711-720, 1992
 A/Title: Expression of a novel FGF in the Xenopus embryo. A new candidate inducing fac
 A/Reference number: S23595; MUID:92315916; PMID:1618138
 A/Accession: S23595
 A/Molecule type: mRNA
 A/Residues: 1-187 <ISA>
 A/Cross-references: EMBL:X62593; NID:964692; PIDN:CAA44479.1; PID:964693
 C/Supersfamily: fibroblast growth factor

Query Match 11.1%; Score 151; DB 2; Length 187;
 Best Local Similarity 31.9%; Pred. No. 2.2e-06;
 Matches 30; Conservative 24; Mismatches 38; Indels 2; Gaps 2;

51 YHLOHKNHVDGAPHOTYSALMIRSEDAFGVITGVMSRRYLCMDRGNIFGSHYFDP 110
 Db FHIQVLPGRINGMHNENRYSLEISPEVGVSLYGIKSAFVAMNKKGLYGRYFN- 133
 75
 111 ENCRFOHTELENGYDVYHSPQY-HFLVSLGRAKR 143
 Db
 134 EECKFKETLLPNNYAYESRKYPGMYIALGKNGR 167

RESULT 12
 150710
 fibroblast growth factor 4 - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C/Accession: S78506; S50858; I50710
 R/Niswander, L.
 submitted to the EMBL Data Library, September 1994
 A/Reference number: S78506
 A/Accession: S78506
 A/Molecule type: DNA
 A/Residues: 1-194 <NTS>
 A/Cross-references: EMBL:U14654; NID:9609347; PIDN:AAA58706.1; PID:9609348
 R/Niswander, L.; Jeffrey, S.; Martin, G.R.; Tickle, C.
 Nature 371, 609-612, 1994
 A/Title: A positive feedback loop coordinates growth and patterning in the vertebrate
 A/Reference number: 150710; MUID:95021713; PMID:7935794
 A/Accession: S50858
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-136, 'O', 137-194, 'I' <NTM>
 A/Cross-references: EMBL:U14654; NID:9609347; PIDN:AAA58706.1; PID:9609348
 C/Genetics:
 A/Gene: FGF4
 C/Supersfamily: fibroblast growth factor
 C/Keywords: growth factor; transforming protein

Query Match 10.8%; Score 146.5; DB 2; Length 194;
 Best Local Similarity 31.1%; Pred. No. 5.9e-06;
 Matches 51; Conservative 22; Mismatches 68; Indels 23; Gaps 7;

3 GARLRWVWVLC--SVCSMSVLR--AYPNASPLIGSSGCGIHYTATANSYHLOHKN 58
 Db GPRQRMDALPAASVAPLPAERDAPADGDLG--YKRLRLY-CNVGIGFHIQVLPD 89
 33
 59 GHVDAEPHOTYSALMIRSEDAFGVITGVMSRRYLCMDRGNIFGSHYFDPENCERFOHQ 118
 Db GRIGIHSENNRYSLEISPEVGVSLYGIKSAFVAMNKKGLYGRYFN- 148
 90
 119 TLENGYDVYHSPQYHFLVSLGRAKR-----FLP 147
 Db
 149 LLPNNYAYESRIYPGMYIALSKNGRTKGNKVSPTMTVTHTFLP 192

RESULT 13
 S20102
 fibroblast growth factor 6 precursor - human
 N/Alternate names: fibroblast growth factor-related protein FGF 6; transforming protei
 C/Species: Homo sapiens (man)
 C/Date: 18-Feb-1994 #sequence_revision 12-Apr-1996 #text_change 21-Jul-2000
 C/Accession: S20102; S23739; S04204; S36910

R;Coulter, F.; Batez, M.; Marice, I.; de Lapeyrière, O.; Birnbaum, D.
 Oncogene 6, 1437-1444, 1991
 A>Title: Putative structure of the FGF6 gene product and role of the signal peptide.
 A/Reference number: S20102; MUID:91360279; PMID:1886714
 A/Accession: S20102
 A>Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-208 <COU>
 A/Cross-references: EMBL:X57075
 A/Note: It is uncertain whether Met-1, Met-11 or Met-34 is the initiator
 R;Iida, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Katoh, O.; Hirohashi, S.; Sato, T.; On
 Oncogene 7, 303-309, 1992
 A>Title: Human hst-2 (FGF-6) oncogene: cDNA cloning and characterization.
 A/Reference number: S23739; MUID:92195660; PMID:1549352
 A/Accession: S23739
 A/Molecule type: mRNA
 A/Residues: 1-208 <IID>
 A/Cross-references: EMBL:X63454
 A/Note: It is uncertain whether Met-1 or Met-11 is the initiator
 R;Marice, I.; Adelaide, J.; Raynaud, F.; Mattei, M.G.; Coulter, F.; Planche, J.; de Lape
 Oncogene 4, 335-340, 1989
 A>Title: Characterization of the HST-related FGF 6 gene, a new member of the fibroblast
 A/Reference number: S04204; MUID:89201880; PMID:2649847
 A/Accession: S04204
 A/Molecule type: DNA
 A/Residues: 81-99, 'G', 101-208 <MAR>
 A/Cross-references: EMBL:X14071; NID:931354; PIDN:CAB37648.2; PID:94467836
 C/Genetics:
 A/Gene: GDB:FGF6; hst-2
 A/Cross-references: GDB:119908; OMIM:134921
 A/Map position: 12P13-12P13
 A/Intons: 115/3; 150/2
 C/Superfamily: fibroblast growth factor
 F,1-40/Domain: (or 11-40 or 34-40) signal sequence #status predicted <SIG>
 F,41-208/Product: fibroblast growth factor 6 #status predicted <MAT>
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 Db 66 AGEIAGVWMSGYLVGIRKQRRLY-CNVGIGPHLVDPGRISGTHEENPYSLEISTIVE 124
 QY 80 AGFVITGVMSRRYLQMPFRGNI FGSHPYDPENCRFQHTLENGDYVHSPOYH----FL 135
 Db 125 RGVVSLFVGYSALFVAMNSKGRVATPSFQ--ECKFRFTLLPNNYNAVESDLYRGTYIAL 183
 QY 136 VSLGRAKRA-----FLP 147
 Db 184 SKYGRVKKRSKVSPIMTVTHFLP 206
 RESULT 14
 S14192
 Fibroblast growth factor 6 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 17-Mar-2000
 C/Accession: S14192; I49665; I49664
 R;de Lapeyrière, O.; Rosnet, O.; Benharroch, D.; Raynaud, F.; Marchetto, S.; Planche, J.
 Oncogene 5, 823-831, 1990
 A>Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.
 A/Reference number: S14192; MUID:90295275; PMID:2193291
 A/Accession: S14192
 A/Molecule type: DNA
 A/Residues: 1-208 <IAP>
 A/Cross-references: EMBL:X51552
 A/Note: It is uncertain whether Met-1 or Met-11 is the initiator
 R;Ollendorff, V.; Rosnet, O.; Marice, I.; Birnbaum, D.; deLapeyrière, O.
 Biochimie 74, 1035-1038, 1992
 A>Title: Isolation and sequence of the murine Fgf6 cDNA.
 A/Reference number: I49664; MUID:93120244; PMID:1477139
 A/Accession: I49665

A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 19-208 <RS>
 A/Cross-references: GB:M92416; NID:9193286; PIDN:AAA62261.1; PID:9666915
 A/Accession: I49664
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-18 <RE2>
 A/Cross-references: GB:M92415; NID:9193286; PIDN:AAA62260.1; PID:9193287
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 A/Gene: Fgf6
 A/Intons: 116/1; 150/3
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 Db 66 AGEIAGVWMSGYLVGIRKQRRLY-CNVGIGPHLVDPGRISGTHEENPYSLEISTIVE 124
 QY 80 AGFVITGVMSRRYLQMPFRGNI FGSHPYDPENCRFQHTLENGDYVHSPOYH----FL 135
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 QY 136 VSLGRAKRA-----FLP 147
 Db 184 SKYGRVKKRSKVSPIMTVTHFLP 206
 RESULT 15
 JC4268
 fibroblast growth factor 4 - bovine
 N/Alternate names: transforming protein hst
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 10-Nov-1995 #sequence revision 08-Feb-1996 #text_change 17-Mar-2000
 C/Accession: JC4268
 R;Yu, J.C.; Desseabra, A.U.J.; Wang, L.M.; Fleming, T.P.; Chedd, M.; Miki, T.; Heidaran
 Gene 162, 333-334, 1995
 A>Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
 A/Reference number: JC4268; MUID:96032369; PMID:7557455
 A/Accession: JC4268
 A/Molecule type: mRNA
 A/Residues: 1-206 <YU>
 A/Cross-references: GB:U15969
 A/Note: The authors translated the codon GGC for residue 114 as Ser
 C/Comment: This protein is a member of fibroblast growth factor family. The hstgene in
 C/Genetics:
 A/Gene: hst
 A/Intons: 113/3; 145/2
 C/Superfamily: fibroblast growth factor
 C/Keywords: thymus; transforming protein
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 Best Local Similarity 32.1%; Pred. No. 3.8e-05;
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 Db 94 FHLQVLDPGRIGVHADTSDLLSIPERGVISIFGVASRFFVAMNSRGRVLSGSPFTTD 153
 QY 111 ENCFQHTLENGDYV---HSPQYHFLVSLGRAKRA-----FLP 147
 Db 154 E-CRFRFTLLPNNYNAECRHPFTALSNGGRVAKGNRVSPTMKVTHFLP 204
 Search completed: May 23, 2003, 07:44:12
 Job time : 21 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: May 23, 2003, 07:43:22 ; Search time 734 Seconds

(without alignments)
33,913 Million cell updates/sec

Title: US-09-901-938-2

Perfect score: 1360

Sequence: 1 MGARLRIMVLCALCSVCSMS.....VNTHAGCTPBGCRPPAKTI 251

Scoring table: BLOSUM62

Searched: 375593 seqs, 99172665 residues

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

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- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1360	100.0	251	9	US-09-992-598-511
3	1360	100.0	251	9	US-09-989-293A-511
4	1360	100.0	251	9	US-09-989-735-511
5	1360	100.0	251	9	US-09-990-444-511
6	1360	100.0	251	9	US-09-989-730-511
7	1360	100.0	251	9	US-09-990-436-511
8	1360	100.0	251	9	US-09-991-181-511
9	1360	100.0	251	9	US-09-993-687-511
10	1360	100.0	251	9	US-09-989-734-511
11	1360	100.0	251	9	US-10-028-072-266
12	1360	100.0	251	9	US-09-997-653-511
13	1360	100.0	251	9	US-10-121-049-266
14	1360	100.0	251	9	US-10-123-804-266
15	1360	100.0	251	9	US-10-140-470-266
16	1360	100.0	251	9	US-09-924-340-26
17	1360	100.0	251	9	US-09-990-438-511
18	1360	100.0	251	9	US-09-990-562-511
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21	1360	100.0	251	9	US-09-997-428-511	Sequence 511, App
22	1360	100.0	251	9	US-09-997-666-511	Sequence 511, App
23	1360	100.0	251	9	US-10-175-746-266	Sequence 266, App
24	1360	100.0	251	9	US-10-176-918-266	Sequence 266, App
25	1360	100.0	251	9	US-10-176-921-266	Sequence 266, App
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27	1360	100.0	251	9	US-10-137-865-266	Sequence 266, App
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30	1360	100.0	251	9	US-10-143-114-266	Sequence 266, App
31	1360	100.0	251	9	US-09-989-726-511	Sequence 511, App
32	1360	100.0	251	9	US-10-140-002-266	Sequence 266, App
33	1360	100.0	251	9	US-09-990-437-511	Sequence 511, App
34	1360	100.0	251	9	US-09-998-156-511	Sequence 511, App
35	1360	100.0	251	9	US-10-142-419-266	Sequence 266, App
36	1360	100.0	251	9	US-09-991-157-511	Sequence 266, App
37	1360	100.0	251	9	US-09-991-172-511	Sequence 511, App
38	1360	100.0	251	9	US-09-997-514-511	Sequence 511, App
39	1360	100.0	251	9	US-09-997-573-511	Sequence 511, App
40	1360	100.0	251	9	US-10-123-262-266	Sequence 266, App
41	1360	100.0	251	9	US-10-142-423-266	Sequence 266, App
42	1360	100.0	251	9	US-09-990-443-511	Sequence 511, App
43	1360	100.0	251	9	US-09-990-726-511	Sequence 511, App
44	1360	100.0	251	9	US-09-997-559-511	Sequence 511, App
45	1360	100.0	251	9	US-09-997-601-511	Sequence 511, App

ALIGNMENTS

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RESULT 1
US-09-901-938-2
; Sequence 2, Application US/09901938
; Patent No. US20020156001A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/09/901,938
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-938-2

Query Match      100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 PEGCRPFAKFI 251
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RESULT 2
US-09-992-598-511
Sequence 511, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Aubertin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhen
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2,1e-123;
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QY 61 VDGAPHQITYSALMTRESDAGFVITGVMSRRYLCAIDFPGNTFGSHYFDPENCRFOHQT 120

DB 61 VDGAPHQITYSALMTRESDAGFVITGVMSRRYLCAIDFPGNTFGSHYFDPENCRFOHQT 120
QY 121 ENGXDYVHSPOYHFLVSLGRARAFPLPGNPPYSQFLSRNEIPLIHNTPIPRRHTRS 180
DB 121 ENGXDYVHSPOYHFLVSLGRARAFPLPGNPPYSQFLSRNEIPLIHNTPIPRRHTRS 180
QY 181 AEDDSERDPLNVLKPRARMTPAAPASCQELPSAEDNSPMAADPLGVYRGGRVNTHAGGTG 240
DB 181 AEDDSERDPLNVLKPRARMTPAAPASCQELPSAEDNSPMAADPLGVYRGGRVNTHAGGTG 240
QY 241 PGCRPFAPKI 251
DB 241 PGCRPFAPKI 251

RESULT 3
US-09-989-293A-511
Sequence 511, Application US/09989293A
Patent No. US2002017164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US/09/989, 293A
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02

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4	PRIOR FILING DATE: 1998-06-03
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69	PRIOR APPLICATION NUMBER: 60/089908

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PRIOR APPLICATION NUMBER:	60/091978
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/092182
PRIOR FILING DATE:	1998-07-09

Query Match	100.0%;	Score 1360;	DB 9;	Length 251;
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Best Local Similarity 100.0%; Pred. No. 2,1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAARLWVCAALCSVCSNSVLRAYPNAPBLGSSWGLIHLTYATARNSYHLQIHKNH 60
Db 1 MGAARLWVCAALCSVCSNSVLRAYPNAPBLGSSWGLIHLTYATARNSYHLQIHKNH 60
QY 61 VDGAHQITYSALMIRSEDAQFVITGVMSRRYLCHDFRGNITGSHYFDPENCRFOHQL 120
Db 61 VDGAHQITYSALMIRSEDAQFVITGVMSRRYLCHDFRGNITGSHYFDPENCRFOHQL 120
QY 121 ENGVDVTHSPQHFLVSLRAKRAFLPGMNPPEYSQLSRNRNPLIHFTPLPRHTTS 180
Db 121 ENGVDVTHSPQHFLVSLRAKRAFLPGMNPPEYSQLSRNRNPLIHFTPLPRHTTS 180
QY 181 AEDDERDPLNVLKPPARMTTPAPASCSOELPSAEDNSPMASDPLGVVGRVTHAGGTG 240
Db 181 AEDDERDPLNVLKPPARMTTPAPASCSOELPSAEDNSPMASDPLGVVGRVTHAGGTG 240
QY 241 PEGCRPPAKFI 251
Db 241 PEGCRPPAKFI 251

RESULT 4
US-09-989-735-511
Sequence 511, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Getber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, O. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301PC61
CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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 PRIOR APPLICATION NUMBER: 60/091633

PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
 Best Local Similarity 100.0%; Pred. No. 2,1e-123;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLARLRLVLCALSCVCSMSVLRAPVNPASPLLGSSWGLIHLHYATANSYHLQIKKHGH 60
 DB 1 MGLARLRLVLCALSCVCSMSVLRAPVNPASPLLGSSWGLIHLHYATANSYHLQIKKHGH 60
 QY 61 VDGAHQITVIALMIRSDAGFVVITGVMSRRYLCPMFRGNI FGSHPDPENCRFQHOTL 120
 DB 61 VDGAHQITVIALMIRSDAGFVVITGVMSRRYLCPMFRGNI FGSHPDPENCRFQHOTL 120
 QY 121 ENGVDVHSPQYHPLVSLGRKRAFLPGMNPYPYSQFLSRNEIPLHNTPIPRRHTS 180
 DB 121 ENGVDVHSPQYHPLVSLGRKRAFLPGMNPYPYSQFLSRNEIPLHNTPIPRRHTS 180
 QY 181 AEDSERDPLNVLKPRAMTPAPASCSQELPSADNSPMASDPLGVYRGVNTAGGTG 240
 DB 181 AEDSERDPLNVLKPRAMTPAPASCSQELPSADNSPMASDPLGVYRGVNTAGGTG 240
 QY 241 PEGCRPFAPKFI 251
 DB 241 PEGCRPFAPKFI 251

RESULT 5 US-09-990-444-511

Sequence 511, Application US/09990444
 Publication No. US20020193300A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Deenoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary B.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gutney, Austin L.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PLC19
 CURRENT APPLICATION NUMBER: US/09/990,444
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12

[illegible]

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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2,1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGARLRWVCLGVCMSVTRAYPNASPLLGSSWGLIHLYTARNSYHLQIHKNGH 60
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QY 61 VDGAHQIYSLMIRSEADGPFVITGVNSRRYLQMDFRGNIFGSHYPDPCRCFOHOTL 120
DB 61 VDGAHQIYSLMIRSEADGPFVITGVNSRRYLQMDFRGNIFGSHYPDPCRCFOHOTL 120
QY 121 ENGVDVNSPOYHFLVLSGRANRAFLPGNNPPYSQFLSRNEIPLIHNTPIPRHTRS 180
DB 121 ENGVDVNSPOYHFLVLSGRANRAFLPGNNPPYSQFLSRNEIPLIHNTPIPRHTRS 180
QY 181 AEDSERPLWVKRANTTPAPASCQELPSAEDNSPAPASPLVYVGRVNTAGGTG 240
DB 181 AEDSERPLWVKRANTTPAPASCQELPSAEDNSPAPASPLVYVGRVNTAGGTG 240
QY 241 PEGCRPPAKFI 251
DB 241 PEGCRPPAKFI 251

RESULT 6
US-09-989-730-511

;; Sequence 511, Application US/09989730
;; Publication No. US20020197674A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrata, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gottlieb, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavich, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2730P1C69
;; CURRENT APPLICATION NUMBER: US/09/989, 730
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
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;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
PRIOR FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 1360; DB 9; Length 251;
 Best Local Similarity 100.0%; Pred. No. 2,1e-123; Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 PEGCRPPAKFI 251
DB 241 PEGCRPPAKFI 251

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RESULT 8
 US-09-991-181-511

Sequence 511, Application US/09991181
 Publication No. US20020197615A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botsstein, David
 APPLICANT: Deenoyers, Luc
 APPLICANT: Baton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Pong, Sherman
 APPLICANT: Gerber, Hanspeter

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APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
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CURRENT FILING DATE: 2001-11-16
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Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2, 1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 AEDDERPPLNVLKPRAMTPAPASCQELPSAEDNSPMASDPLGVVVGGRVNTAGGTG 240
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DB 241 PEGCRPAKFI 251

RESULT 9
US-09-993-687-511
; Sequence 511, Application US/09993687
; Publication No. US20020198149A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Tamas, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
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PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090252
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PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
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PRIOR APPLICATION NUMBER: 60/090472
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PRIOR APPLICATION NUMBER: 60/090540
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PRIOR APPLICATION NUMBER: 60/090542
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2,1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARLRWVCLGVCNSVTRAPNAPPLGSSWGLIHTATARNSTHLQHKNH 60
DB 1 MGARLRWVCLGVCNSVTRAPNAPPLGSSWGLIHTATARNSTHLQHKNH 60
QY 61 VDGARHQTYSALMTBSRDEAGFVITGVMSRRYLCDPFGNIFGSHYFPEHCROHQT 120
DB 61 VDGARHQTYSALMTBSRDEAGFVITGVMSRRYLCDPFGNIFGSHYFPEHCROHQT 120
QY 121 ENGVDVYSPQYHFLVSLGRARAFPLPGNNPPYQSQFLSRREIPIIHNTPIPRRTS 180
DB 121 ENGVDVYSPQYHFLVSLGRARAFPLPGNNPPYQSQFLSRREIPIIHNTPIPRRTS 180
QY 181 AEDDERPPLNLTKPRARNTTPASCSQELPSAEDNSPMAADPLGVVGRGVNTAGGTG 240
DB 181 AEDDERPPLNLTKPRARNTTPASCSQELPSAEDNSPMAADPLGVVGRGVNTAGGTG 240

QY 241 PEGCRPAKFI 251
DB 241 PEGCRPAKFI 251

RESULT 10
US-09-989-734-511
Sequence 511, Application US/09989734
Publication No. US2003003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrata, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Aubin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C64
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,734
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/088734
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/090355
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090863
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PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2,1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MUGAARLWVLCALCVCSNSTRAYPNASPLIGSSWGLIHLTYTARNSTYHLQHKNGH 60
DB 1 MUGAARLWVLCALCVCSNSTRAYPNASPLIGSSWGLIHLTYTARNSTYHLQHKNGH 60
QY 61 VDGAPHTTYSALMTRSSDAGFVVITGMSRRYLQMDRGNIFGSHYDPEHCROHOTL 120
DB 61 VDGAPHTTYSALMTRSSDAGFVVITGMSRRYLQMDRGNIFGSHYDPEHCROHOTL 120

QY 121 ENGYNVHSPQYHFLVSLGRKRAFLPGNPPYQFLSRNFIPLIHNTPIPRHTRS 180
| | | | |
Db 121 ENGYNVHSPQYHFLVSLGRKRAFLPGNPPYQFLSRNFIPLIHNTPIPRHTRS 180
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QY 181 AEDSEBDLNTLKPRAWTPAPASCSOELPSAEDNSPMASDPLGVNRCRVNTHAGTG 240
| | | | |
Db 181 AEDSEBDLNTLKPRAWTPAPASCSOELPSAEDNSPMASDPLGVNRCRVNTHAGTG 240
| | | | |
QY 241 PEGCRPFAKFI 251
| | | | |
Db 241 PEGCRPFAKFI 251
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RESULT 11
US-10-028-072-266
; Sequence 266, Application US/10028072
; Publication No. US2003000411A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
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; PRIOR APPLICATION NUMBER: 60/063127
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/081203
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081695
; PRIOR FILING DATE: 1998-04-14

PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-12
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/090349
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PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
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PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2,1e-123;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARLRIMVCAICGVCSMSVIRAYPNASPLIGSSWGLIHLYTATARNSYHLQIHKNGH 60
Db 1 MGARLRIMVCAICGVCSMSVIRAYPNASPLIGSSWGLIHLYTATARNSYHLQIHKNGH 60

Qy 61 VDGAPHQITTSALMTRSDAGFVITGVMSRRLICMDRGNIFGSHYPPENCRRQHQTL 120
Db 61 VDGAPHQITTSALMTRSDAGFVITGVMSRRLICMDRGNIFGSHYPPENCRRQHQTL 120

Qy 121 ENGVDVNSPOYHFLVSGRAKRAFLPGMNPYPYSQFLSRREIPLIHNTPIPRHTRS 180
Db 121 ENGVDVNSPOYHFLVSGRAKRAFLPGMNPYPYSQFLSRREIPLIHNTPIPRHTRS 180

Qy 181 AEDSERDPLNVLKPRAMTPAPASCQELPSAEDNSPMASDPLGVGRVNTAGGTG 240
Db 181 AEDSERDPLNVLKPRAMTPAPASCQELPSAEDNSPMASDPLGVGRVNTAGGTG 240

Qy 241 PEGCRPFPAKFI 251
Db 241 PEGCRPFPAKFI 251

RESULT 12
US-09-997-653-511
Sequence 511, Application US/09997653
Publication No. US20030008297A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC38
CURRENT APPLICATION NUMBER: US/09/997, 653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

[illegible]

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2,1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARLRMLVWCLGVCVSNVLRAYVNAAPLLGSSWGGIHLHYTATARNYHLQIKNGH 60
DB 1 MGARLRMLVWCLGVCVSNVLRAYVNAAPLLGSSWGGIHLHYTATARNYHLQIKNGH 60
QY 61 VDGARHQTITSLMTRESBAGVVTITGVNSRRYLCDPFGNIFGSHYFDPENCRFQHTL 120
DB 61 VDGARHQTITSLMTRESBAGVVTITGVNSRRYLCDPFGNIFGSHYFDPENCRFQHTL 120
QY 121 ENGVDVHSPQVHFLVSLGRARAFIPGNPPYISQFLSRNHEIPLIHNTPIPRHRTS 180
DB 121 ENGVDVHSPQVHFLVSLGRARAFIPGNPPYISQFLSRNHEIPLIHNTPIPRHRTS 180
QY 181 AEDSERDPLNVLKPRARMTAPASCOSLPASADNSPMAADPLGVNRCGRVNTAGGTG 240
DB 181 AEDSERDPLNVLKPRARMTAPASCOSLPASADNSPMAADPLGVNRCGRVNTAGGTG 240
QY 241 PEGCRPFAPFI 251
DB 241 PEGCRPFAPFI 251

RESULT 13
US-09-993-667-511

Sequence 511, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P104
CURRENT APPLICATION NUMBER: US/09/993,667
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16

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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478

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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 1360; DB 9; Length 251;
 Best Local Similarity 100.0%; Pred. No. 2, Le-123;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGAARLRLMVCALCSGCSMSVLRAPNAPSPLGSSWGLIHLXTTANSTYHLQHKXGH 60
QY 61 VDGAPHOTIYSALMIRSADAGFVITGVMSRRYLQMDPRGNIFGSHYFDPENCRFQHOTL 120
DB 61 VDGAPHOTIYSALMIRSADAGFVITGVMSRRYLQMDPRGNIFGSHYFDPENCRFQHOTL 120
QY 121 ENGVDVHSPQYHFLVLSGRKRAFLPGMNPYPYQFLSRNRIPLIHNTPIPRRHTRS 180
DB 121 ENGVDVHSPQYHFLVLSGRKRAFLPGMNPYPYQFLSRNRIPLIHNTPIPRRHTRS 180
QY 161 AEDDERPPLNVLKPRAMTPAPASCSEQLPSAENSPMASDPLGVNAGRVNTAGGTG 240
DB 161 AEDDERPPLNVLKPRAMTPAPASCSEQLPSAENSPMASDPLGVNAGRVNTAGGTG 240
QY 241 PEGCRPFPAFI 251
DB 241 PEGCRPFPAFI 251

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RESULT 14
US-10-121-049-266
Sequence 266, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 266
LENGTH: 251
TYPE: PRT

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ORGANISM: Homo Sapien
US-10-121-049-266

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARLRWVCLCSVCSMSVLRAYPNASPLIGSSWGGILHLYTATARNSYHLQIHKNGH 60
DB 1 MGARLRWVCLCSVCSMSVLRAYPNASPLIGSSWGGILHLYTATARNSYHLQIHKNGH 60
QY 61 VDGAHQITISALMIRSEBAGFVITGVMSRRYLICMDFRGNIFGSHYFDPENCRFQHOTL 120
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QY 121 ENGVDVYHSPQYHFLVSLGRAKRAFLPGNPPYSGFLSRRNEIPLIHNTPIPRRHTS 180
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QY 241 PEGCRPPAKFI 251
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RESULT 15

US-10-123-904-266
Sequence 266, Application US/10123904
Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godoweki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 266
LENGTH: 251
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-266

Query Match 100.0%; Score 1360; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARLRWVCLCSVCSMSVLRAYPNASPLIGSSWGGILHLYTATARNSYHLQIHKNGH 60
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QY 61 VDGAHQITISALMIRSEBAGFVITGVMSRRYLICMDFRGNIFGSHYFDPENCRFQHOTL 120
DB 61 VDGAHQITISALMIRSEBAGFVITGVMSRRYLICMDFRGNIFGSHYFDPENCRFQHOTL 120

DB 61 VDGAHQITISALMIRSEBAGFVITGVMSRRYLICMDFRGNIFGSHYFDPENCRFQHOTL 120
QY 121 ENGVDVYHSPQYHFLVSLGRAKRAFLPGNPPYSGFLSRRNEIPLIHNTPIPRRHTS 180
DB 121 ENGVDVYHSPQYHFLVSLGRAKRAFLPGNPPYSGFLSRRNEIPLIHNTPIPRRHTS 180
QY 181 AEDDSERDPLNTLKPRARMTTPAPASCSQELPSAEDNSPMASDPLGVVRCGRVNTHAGTGTG 240
DB 181 AEDDSERDPLNTLKPRARMTTPAPASCSQELPSAEDNSPMASDPLGVVRCGRVNTHAGTGTG 240
QY 241 PEGCRPPAKFI 251
DB 241 PEGCRPPAKFI 251

Search completed: May 23, 2003, 07:58:43
Job time : 736 secs

GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2003, 07:41:52 ; Search time 29 seconds

(without alignments)
254.660 Million cell updates/sec

Title: US-09-901-938-2

Perfect score: 1360

Sequence: 1 MEGARLRLWTCALCVCVMS.....VNHAGTGTGCGCRPAKFI 251

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	182.5	13.4	245	2	US-08-867-471-11
3	182.5	13.4	245	2	US-08-438-439C-7
4	182.5	13.4	240	4	US-09-417-721-7
5	180.5	13.3	239	1	US-08-464-590A-11
6	180.5	13.3	239	1	US-08-462-169B-11
7	180.5	13.3	239	2	US-08-207-412B-14
8	180.5	13.3	239	2	US-08-951-822-35
9	180.5	13.3	239	3	US-09-103-079-11
10	180.5	13.3	239	3	US-08-718-904-12
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13	180.5	13.3	239	4	US-09-368-951-35
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16	176	12.9	183	4	US-08-776-207-15
17	176	12.9	183	4	US-09-507-773-15
18	176	12.9	183	5	PCT-US95-09172-15
19	175.5	12.9	245	3	US-08-705-245-12
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21	171	12.6	241	6	5175383-7
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24	169	12.4	267	3	US-09-103-079-13
25	168.5	12.4	247	4	US-09-240-952-5
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30	168.5	12.4	268	2	US-08-867-471-12	Sequence 8, Appl
31	168.5	12.4	268	2	US-08-438-439C-8	Sequence 33, Appl
32	168.5	12.4	268	2	US-08-951-822-33	Sequence 14, Appl
33	168.5	12.4	268	3	US-08-718-904-14	Sequence 15, Appl
34	168.5	12.4	268	3	US-09-023-082A-15	Sequence 17, Appl
35	168.5	12.4	268	3	US-09-093-585-17	Sequence 14, Appl
36	168.5	12.4	268	4	US-09-240-952-2	Sequence 33, Appl
37	168.5	12.4	268	4	US-09-368-951-33	Sequence 18, Appl
38	167.5	12.3	268	3	US-08-705-245-13	Sequence 18, Appl
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40	156	11.5	266	6	5175383-5	Sequence 18, Appl
41	154	11.3	158	4	US-08-776-207-18	Sequence 18, Appl
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43	153.5	11.3	219	1	US-08-441-629-13	Sequence 13, Appl
44	153.5	11.3	219	3	US-08-776-207-13	Sequence 13, Appl
45	153.5	11.3	219	4	US-09-507-773-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-08-439-725A-11
Sequence 11, Application US/08439725A
Patent No. 5693775
GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (PHF-1) AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,725A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 617/678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-439-725A-11
Query Match 13.4%; Score 182.5; DB 1; Length 245;
Best Local Similarity 29.4%; Pred. No. 6; 7e-12;
Matches 63; Conservative 26; Mismatches 88; Indels 37; Gaps 8;
QY 42 LVTATATNSYHLOIHKNHGVDGAPHOTIYSALMIRSDAGFVVITGMSRRYICMPFGN 101
DB 48 LVCAI---KHHQDHSGRVNSLNSAIVSILEITAVEGVVAIKGLFSGRIYLAANKRGR 104

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QY 102 IFSGHYFDPENCROHQTLENGYDVYHSPOYHFLVSLGAKRAFLPGMNP----- 152
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Db 162 RPRGFRTKRTQKSLF----LPRVLGHKHDMVRLLOSQPRAPBEGSQPROR----- 211
QY 205 SCQGLPSAEDNSPMASDPLGVGRGVNTHAG 238
Db 212 --ROKKOSPDHGM--ETLSTRATPSTQHTGG 241

RESULT 2
US-08-867-471-11
Sequence 11, Application US/08867471
Patent No. 5872226
GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,471
FILING DATE: 02-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/439,725
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/047001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 617/678-5099
INFORMATION FOR SEO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-867-471-11

Query Match 13.4%; Score 182.5; DB 2; Length 245;
Best Local Similarity 29.4%; Pred. No. 6,7e-12;
Matches 63; Conservative 26; Mismatches 88; Indels 37; Gaps 8;

QY 42 LYTATANSTHLOIHKKGVDAAPHOTIYSALMIRSEDAFVITGVMSRRYLCMDPRGN 101
Db 48 LYCAT--KTHLOLHPSGRVNSLENSAYSILEITAVEGVVAIKGLFSGRYLAMNKRGR 104
QY 102 IFSGHYFDPENCROHQTLENGYDVYHSPOYHFLVSLGAKRAFLPGMNP----- 152
Db 105 LVASDHVNAE-CEVERIHELGYNTYASRLYRTGSSGPGAQRO--PGAORPWYVSVNGK 161
QY 153 -PYSQFLSRNEIPLIHNTPIPR-----RHTRSAEDSERDPLNVLKPRAMTPAPA 204
Db 212 --ROKKOSPDHGM--ETLSTRATPSTQHTGG 241

Db 162 RPRGFRTKRTQKSLF----LPRVLGHKHDMVRLLOSQPRAPBEGSQPROR----- 211
QY 205 SCQGLPSAEDNSPMASDPLGVGRGVNTHAG 238
Db 212 --ROKKOSPDHGM--ETLSTRATPSTQHTGG 241

RESULT 3
US-08-438-439C-7
Sequence 7, Application US/08438439C
Patent No. 5876967
GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,439C
FILING DATE: May 12, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-439C-7

Query Match 13.4%; Score 182.5; DB 2; Length 245;
Best Local Similarity 29.4%; Pred. No. 6,7e-12;
Matches 63; Conservative 26; Mismatches 88; Indels 37; Gaps 8;

QY 42 LYTATANSTHLOIHKKGVDAAPHOTIYSALMIRSEDAFVITGVMSRRYLCMDPRGN 101
Db 48 LYCAT--KTHLOLHPSGRVNSLENSAYSILEITAVEGVVAIKGLFSGRYLAMNKRGR 104
QY 102 IFSGHYFDPENCROHQTLENGYDVYHSPOYHFLVSLGAKRAFLPGMNP----- 152
Db 105 LVASDHVNAE-CEVERIHELGYNTYASRLYRTGSSGPGAQRO--PGAORPWYVSVNGK 161
QY 153 -PYSQFLSRNEIPLIHNTPIPR-----RHTRSAEDSERDPLNVLKPRAMTPAPA 204
Db 162 RPRGFRTKRTQKSLF----LPRVLGHKHDMVRLLOSQPRAPBEGSQPROR----- 211
QY 205 SCQGLPSAEDNSPMASDPLGVGRGVNTHAG 238
Db 212 --ROKKOSPDHGM--ETLSTRATPSTQHTGG 241

RESULT 4

US-09-417-721-7
; Sequence 7, Application US/09417721
; Patent No. 6451303
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha J.
; APPLICANT: Kavanaugh, Michael W.
; TITLE OF INVENTION: Angiotensin II Receptor Antagonists
; TITLE OF INVENTION: Administering
; FILE REFERENCE: 1296/12169US05
; CURRENT APPLICATION NUMBER: US/09/417,721
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/104,103
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO: 7
; LENGTH: 240
; TYPE: PR
; ORGANISM: Murine FGF-3
US-09-417-721-7
Query Match 13.4%; Score 182; DB 4; Length 240;
Best Local Similarity 28.7%; Pred. No. 7.4e-12;
Matches 56; Conservative 26; Mismatches 69; Indels 42; Gaps 7;
QY 42 LYRTAANSYHLQHKNGHVDGAPHOTIYSALMIRSEDAGFVITGVMSRRLCMDFRGN 101
DB 48 LYCAT--KXHLQHPGSRVNGSLNSAYSLITAVGVVAIKGLFSGRYLANNKRG 104
QY 102 IFGSHYFDPENCRCFOHQTLENGYDVHSPQYHFLVSL--GRAKRFLPGMNP--P 153
DB 105 LYASDHYNAB-CEFEVERIHELGYNTVYASRLYRTVSTPGARQPSAERLWTVSVNGKGR 163
QY 153 -PYSQFLSRNE--IPLIHFNTP-----IPRHRSAEDDSER 187
DB 162 RPRRGFTTRKQKSLPLPRVLGHKDHVMVLLSSQPRAPGSGQPRQRKQSPGDH 221
QY 188 DPLNVLKPRARMTPA 202
DB 222 GKMETLSTRA--TPS 234
RESULT 5
US-08-464-590A-11
; Sequence 11, Application US/08464590A
; Patent No. 5763214
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,590A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J. G.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 325800-438
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-590A-11
Query Match 13.3%; Score 180.5; DB 1; Length 239;
Best Local Similarity 31.0%; Pred. No. 1.1e-11;
Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;
QY 42 LYRTAANSYHLQHKNGHVDGAPHOTIYSALMIRSEDAGFVITGVMSRRLCMDFRGN 101
DB 48 LYCAT--KXHLQHPGSRVNGSLNSAYSLITAVGVVAIKGLFSGRYLANNKRG 104
QY 102 IFGSHYFDPENCRCFOHQTLENGYDVHSPQYHFLVSL--GRAKRFLPGMNP--P 153
DB 105 LYASEHYSAB-CEFEVERIHELGYNTVYASRLYRTVSTPGARQPSAERLWTVSVNGKGR 163
QY 154 YSGLSRNEIPLIHFNTPIPRH--TRSAEDDSERDPLNVLKPRAR 198
DB 164 RRGFTTRKQKSLPLPRVLGHKDHVMVLLSSQPRAPGSGQPRQRKQSPGDH 221
RESULT 6
US-08-462-169B-11
; Sequence 11, Application US/08462169B
; Patent No. 5773252
; GENERAL INFORMATION:
; APPLICANT: John Greene and Craig A. Rosen
; TITLE OF INVENTION: Fibroblast Growth Factor-15
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,169B
; FILING DATE: 05 JUN 95
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J. G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-441 (PR203)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-462-169B-11
Query Match 13.3%; Score 180.5; DB 1; Length 239;
Best Local Similarity 31.0%; Pred. No. 1.1e-11;
Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

Db 164 RRGFKTRRTQKSSLFPLPRVLDRHDEHWRQJQSGLPFRPGKGVQPRRR 211

RESULT 10

US-08-718-904-12
Sequence 12, Application US/08718904
Patent No. 6037329

GENERAL INFORMATION:

APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6037329tendburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= "FGF-3"

US-08-718-904-12

Query Match 13.3%; Score 180.5; DB 3; Length 239;
Best Local Similarity 31.0%; Pred. No. 1,1e-11;
Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

QY 42 LYTATARNSTHLOHKNKHGHDGAPHOTIYSALMIRSEDAAGVVTGVMSSRYLCMPDRGN 101
DB 48 LYCAT--KTHLOHPSGRVNGSIENSAYSILITAVEGIVAIRGFSGRYLLMNRGR 104
QY 102 IFSGSHYFDPENCRFQHOTLENGVDVYHSPQYHFLVSL-----GRAKRAFLPGMNP--P 153
DB 105 LVASHEHYSAB-CERVEIHELGLVITVSRKYRTYSTPGARQPSAEMLMVSYNGKGRP 163
QY 154 YSQFLSRNREIPLIHFTPIPRR--TRSAEDSEBDPLNLKPRAR 198
DB 164 RRGFKTRRTQKSSLFPLPRVLDRHDEHWRQJQSGLPFRPGKGVQPRRR 211

RESULT 11

US-09-023-082A-21
Sequence 21, Application US/09023082A

GENERAL INFORMATION:

APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE

APPLICANT: RAMPEY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein

US-09-023-082A-21

Query Match 13.3%; Score 180.5; DB 3; Length 239;
Best Local Similarity 31.0%; Pred. No. 1,1e-11;
Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

QY 42 LYTATARNSTHLOHKNKHGHDGAPHOTIYSALMIRSEDAAGVVTGVMSSRYLCMPDRGN 101
DB 48 LYCAT--KTHLOHPSGRVNGSIENSAYSILITAVEGIVAIRGFSGRYLLMNRGR 104
QY 102 IFSGSHYFDPENCRFQHOTLENGVDVYHSPQYHFLVSL-----GRAKRAFLPGMNP--P 153

Db 105 LYASEHSAB-CEFEVERIHEIGNTYASRLYTVSSTPGARQPSAEKLMVSVNGKGRP 163
QY 154 YSOFLSRNEIPLIHFTPIPRH--TRSAEDSEDPPLNVLKPRAR 198
Db 164 RRGFKTRTKQSSFLPRVLDHRDHENVRQLOSGLPREPCKGVOPRRR 211

RESULT 12
US-09-093-585-11
; Sequence 11, Application US/09093585
; Patent No. 6110893
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/093,585
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/464,590
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J. G.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 325800-438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-093-585-11

Query Match 13.3%; Score 180.5; DB 3; Length 239;
Best Local Similarity 31.0%; Pred. No. 1.1e-11;
Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

QY 42 LYTAANSYHLQHKNGVDGAPHOITYSALMIRSEDAGFVITGVMSRRYLCMDPRGN 101
Db 48 LYCAT--KYHLQHPGSRVGSLENSAYSLIETAVGVIAIRGLSGRIANMKGR 104
QY 102 IFGSHYFPENCROHQTLNGVDVHSPQYHFLVSL-----GRAKAFLEGNMP--P 153
Db 105 LYASEHSAB-CEFEVERIHEIGNTYASRLYTVSSTPGARQPSAEKLMVSVNGKGRP 163
QY 154 YSOFLSRNEIPLIHFTPIPRH--TRSAEDSEDPPLNVLKPRAR 198
Db 164 RRGFKTRTKQSSFLPRVLDHRDHENVRQLOSGLPREPCKGVOPRRR 211

RESULT 13
US-09-368-951-35
; Sequence 35, Application US/09368951

; Patent No. 6352971
; GENERAL INFORMATION:
; APPLICANT: Delsher, Theresa A.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Raymond, Fennella C.
; APPLICANT: Bukowski, Thomas R.
; APPLICANT: Holderman, Susan D.
; APPLICANT: Hansen, Birgit
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20
; CURRENT APPLICATION NUMBER: US/09/368,951
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 08/951,822
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-368-951-35

Query Match 13.3%; Score 180.5; DB 4; Length 239;
Best Local Similarity 31.0%; Pred. No. 1.1e-11;
Matches 52; Conservative 26; Mismatches 75; Indels 15; Gaps 5;

QY 42 LYTAANSYHLQHKNGVDGAPHOITYSALMIRSEDAGFVITGVMSRRYLCMDPRGN 101
Db 48 LYCAT--KYHLQHPGSRVGSLENSAYSLIETAVGVIAIRGLSGRIANMKGR 104
QY 102 IFGSHYFPENCROHQTLNGVDVHSPQYHFLVSL-----GRAKAFLEGNMP--P 153
Db 105 LYASEHSAB-CEFEVERIHEIGNTYASRLYTVSSTPGARQPSAEKLMVSVNGKGRP 163
QY 154 YSOFLSRNEIPLIHFTPIPRH--TRSAEDSEDPPLNVLKPRAR 198
Db 164 RRGFKTRTKQSSFLPRVLDHRDHENVRQLOSGLPREPCKGVOPRRR 211

RESULT 14
US-08-438-439C-17
; Sequence 17, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-439C-17

Query Match 13.3%; Score 180.5; DB 2; Length 245;
Best Local Similarity 28.0%; Pred. No. 1.1e-11;
Matches 70; Conservative 29; Mismatches 104; Indels 47; Gaps 10;

QY 19 MSVLR-AYPNAP-----LIGSSWGLIHLTYATAR-----NSYHQLKNGHVDAP 65
DB 9 LSLLEPPTPTGPTGLRLRDAGRGVYEHLGAPRRKLYCATKYLQLHPSGRVNSL 68
QY 66 HQTYSALMIRSEDAGFVITGVMSRRYLQMDFRGNIFGSHYFPDPENCFOHQTLENGYD 125
DB 69 ENSAYSLILEITAVEGVVIAIKGLFSGRYLANKKGRLYASDHVNAE-CEFERIHELGYN 127
QY 126 VYHSPOYHPLVSLGRAKAFLPGMNP-----PYSQFLSRNEIPLIHNTPIPR 175
DB 128 TYASRLYRTGSSGPGARQ--PGAQRPYVYVNGKGRPRRGFKTRRTQKSLF---LPR 181
QY 176 -----RHTRSADSESDPDLNVLKPRARMTAPASGSELPAEDNSPMASDPLGYVR 228
DB 182 VLGHKHENYRLLOSQPRAPGEGSOPRQ-----RQKQSGPDHGKM--ETLSTRA 231
QY 229 GGRVNTAGG 238
DB 232 TPSTQLHTGG 241

RESULT 15
US-08-441-629-15

/ Sequence 15, Application US/08441629
/ Patent No. 5766923

/ GENERAL INFORMATION:

/ APPLICANT: Kirschner, Marc W.

/ APPLICANT: Kinoshita, No. 57669231yuki

/ TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY

/ NUMBER OF SEQUENCES: 17

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

/ STREET: Two Militia Drive

/ CITY: Lexington

/ STATE: Massachusetts

/ COUNTRY: USA

/ ZIP: 02173

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent in Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/441,629

/ FILING DATE: 15-MAY-1995

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/279,217

/ FILING DATE: 22-JUL-1994

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Granahan, Patricia

/ REGISTRATION NUMBER: 32,227

/ TELEPHONE: (617) 861-6240

/ TELEFAX: (617) 861-9540

/ INFORMATION FOR SEQ ID NO: 15:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 183 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-629-15

Query Match 12.9%; Score 176; DB 1; Length 183;
Best Local Similarity 35.6%; Pred. No. 2.2e-11;
Matches 47; Conservative 19; Mismatches 50; Indels 16; Gaps 4;

QY 42 LYTAANSTYHLQIHKNHVDGAPHOQITYSALMIRSEDAGFVITGVMSRRYLQMDFRGN 101
DB 48 LYCAT--KYHLQLHPSGRVNSLENGAYSLILEITAVEGVVIAIKGLFSGRYLANKKRGR 104
QY 102 IFGSHYDPENCROHQTLENGYDVYHSPOYHPLVSLGRAKAFLPGMNP----- 152
DB 105 LYASDHVNAE-CEFERIHELGYNTASRLYRTGSSGPGARQ--PGAQRPYVYVNGKGR 161
QY 153 -PYSQFLSRNE 163
DB 162 RPRRGFKTRRTQ 173

Search completed: May 23, 2003, 07:46:21
Job time : 31 secs

XX	PR	04-OCT-2000; 2000US-0237963.
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	PA	(SMIK) SMITHKLINE BEECHAM PLC.
XX	P1	Agarwal P, Kabnick KS, Murdoch FR, Rivvi SK, Smith RF, Xiang Z;
XX	DR	WPI; 2001-536566/59.
XX	DR	N-P8DB; AAD16366.
XX	PT	New secreted and membrane associated polypeptides for treating
XX	PT	Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
XX	PT	disorders, stroke, and asthma
XX	PS	Claim 1; Page 91; 94pp; English.
XX	XX	The present sequence is a human sdbpgf-19b protein,
XX	XX	a secreted protein of the invention.
XX	CC	The invention relates to secreted and membrane associated polypeptides
XX	CC	and nucleic acid molecules encoding such polypeptides. Sequences of the
XX	CC	invention are useful for treating diseases such as Alzheimer's disease,
XX	CC	amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases
XX	CC	of the immune system, haematopoietic disease, inflammation, anxiety,
XX	CC	schizophrenia, feeding disorders, anorexia, depression, social, sexual
XX	CC	and rewarded behaviour, cardiovascular disease, sleep disorder, learning
XX	CC	and memory alteration and altered immune response, seizure, migraine,
XX	CC	cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment
XX	CC	of transsexuals, growth abnormalities, obesity, infections, autoimmune
XX	CC	diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,
XX	CC	disorders associated with healthy maintenance of gastric mucosa and
XX	CC	repair of acute and chronic mucosal lesion, lung carcinoma, cerebral
XX	CC	ischemia, atherosclerosis, cirrhosis, Huntington's disease, headache,
XX	CC	amestia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy,
XX	CC	congestive heart failure, cardiac arrhythmias, hypercholesterolemia,
XX	CC	viral and non-viral hepatitis, type I and type II diabetes mellitus,
XX	CC	glomerulonephritis, renovascular hypertension, hypoglycaemia, periodic
XX	CC	paralyses, tendinitis and malignant hyperthermia. Polypeptides of the
XX	CC	invention are used to identify membrane bound and soluble receptors.
XX	CC	They are also useful as vaccines for inducing an immunological response
XX	CC	in a mammal. Polynucleotides of the invention are used in gene therapy.
XX	CC	They are also valuable for chromosome localisation studies and tissue
XX	CC	expression studies.
SQ	Sequence	251 AA;
Query Match	100.0%; Score 1360; DB 22; Length 251;	
Best Local Similarity	100.0%; Pred. No. 7.5e-131;	
Matches 251; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1 MGAAIRLWVCAICGVCSMSVLRAVENAPLLGSSWGGLIHLYTATARNSYHLQIKNKH	60
Db	1 MGAIRLRWVCAICGVCSMSVLRAYENAPLLGSSWGGLIHLYTATARNSYHLQIKNKH	60
QY	61 VDGARHQTITYSALMTRSEBAGFVVITGVNSRRLCMDFPGNIFGSHPDPENCRFQHQL	120
Db	61 VDGAHQITITYSALMTRSEBAGFVVITGVNSRRLCMDFPGNIFGSHPDPENCRFQHQL	120
QY	121 ENGIVVYHSPOHFVLSLRARAKAFIPGNPPPYSGFLSRBNETLIHNTPIPRHHTS	180
Db	121 ENGIVVYHSPOHFVLSLRARAKAFIPGNPPPYSGFLSRBNETLIHNTPIPRHHTS	180
QY	181 AEDDERDPLNTLKPRARTTPASPASCOELPSAENDSPASDPLGVVRGARVNTHAGTG	240
Db	181 AEDDERDPLNTLKPRARTTPASPASCOELPSAENDSPASDPLGVVRGARVNTHAGTG	240
QY	241 PEGCRPFPAFT 251	
Db	241 PEGCRPFPAFT 251	
RESULT 2		
AAB85810		
ID	AAB85810 standard; Protein; 251 AA.	

XX	AA865610;
AC	
XX	
DT	29-OCT-2001 (first entry)
XX	
DE	Human fibroblast growth factor (FGF)-23.
XX	
KW	Fibroblast growth factor; FGF; FGF-23; osteopathic; vulnerability; ADHR;
KM	hepatotropic; autosomal dominant hypophosphatemic rickets; human;
XX	angiogenesis; gene-therapy; liver disorder; anticense-therapy.
OS	Homo sapiens.
XX	
FT	Key
FT	Peptide
FT	Protein
XX	
PV	MO200161007-A2.
PD	
PD	23-AUG-2001.
XX	
PE	15-FEB-2001; 2001WO-US04778.
PR	15-FEB-2000; 2000US-0182442.
PR	20-APR-2000; 2000US-0198903.
PR	15-FEB-2001; 2001US-0748581.
PA	(AMGE-) AMGEN INC.
PI	Luethy R, Yang R, Suggs S, Sarosi D;
DR	WPI; 2001-514774/56.
DR	N-PSDB; AAH76317.
XX	
PT	An isolated nucleic acid molecule encoding a fibroblast growth factor
PT	23 useful for treating autosomal dominant hypophosphatemic rickets -
PS	Claim 15; Fig 1A-B; 158bp; English.
XX	
CC	This represents a human fibroblast growth factor (FGF)-23 polypeptide.
CC	The DNA insert is contained in ATCC Deposit No. PTA-1617. FGF-23 can be
CC	expressed by standard recombinant methodology. The FGF-23 polypeptides,
CC	polynucleotides, modulators and antibodies are useful for treating,
CC	preventing, or ameliorating an FGF-23 polypeptide-related disease,
CC	condition or disorder especially autosomal dominant hypophosphatemic
CC	rickets (ADHR). They are also useful for diagnosing a pathological
CC	condition and/or stimulating angiogenesis, promoting wound healing and
CC	treating disorders of the liver.
SQ	Sequence 251 AA;
XX	
Query Match	100.0%; Score 1360; DB 22; Length 251;
Best Local Similarity	100.0%; Pred. No. 7.5e-131;
Matches 251, Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 MLGARLRMLWCALSCVCSMSVTRAYPNASPLLGSSWGCLIHLYTNTANSHLOHKNGH 60
Db	1 MLGARLRMLWCALSCVCSMSVTRAYPNASPLLGSSWGCLIHLYTATAENSHLQTHKNGH 60
OY	61 VDGAPHQTITGALMIRSEDAAGFVVITGVMSRRYLCPMDPRNIPGSHYDPENCRCFOHTL 120
Db	61 VDGAPHQTITGALMIRSEDAAGFVVITGVMSRRYLCPMDPRNIPGSHYDPCNCRCFOHTL 120
OY	121 ENGIDVTHSPDYHFLVLSIGRAKRAFLLPGMNDPPYSOFLSRNEIPLIHFNTPIPRRHRS 180
Db	121 ENGIDVTHSPDYHFLVLSIGRAKRAFLLPGMNDPPYSOFLSRNEIPLIHFNTPIPRRHRS 180
OY	181 AEDDSERPLVLVLPRAMTAPASCCELEPSADNSPMAADPLGVVGCGVNTHAGTG 240
Db	181 AEDDSERPLVLVLPRAMTAPASCCELEPSADNSPMAADPLGVVGGRVNHAGTG 240

QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 3
 AAG63944
 ID AAG63944 standard; Protein; 251 AA.

AC AAG63944;

DT 29-OCT-2001 (first entry)

DE Amino acid sequence of human fibroblast growth factor 23 (FGF-23).

KW Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer;
 KW congenital defect; fertility; abnormal growth; thymus function;
 KW leukemia; lymphoma; autoimmune disease; proliferative disorder;
 KW differentiation disorder; central nervous system disorder; infarction;
 KW Parkinson's disease; Alzheimer's disease; Crohn's disease; inflammation;
 KW intestinal wound; motility disorder; absorption disorder; stroke;
 KW congenital malformation; ischemic vascular disease; myocardial ischemia;
 KW peripheral vascular disease; renal artery disease; bone disease;
 KW musculoskeletal disease; skeletal myopathy; arthritis.

OS Homo sapiens.

PN WO200166596-A2.

PD 13-SEP-2001.

PF 07-MAR-2001; 2001WO-US07469.

PR 08-MAR-2000; 2000US-0187854.

PR 18-SEP-2000; 2000US-0233368.

PR 05-DEC-2000; 2000US-0251649.

PA (CHIR) CHIRON CORP.

PA (KYOU) UNIV KYOTO.

PI Itoh N, Kavanagh MW;

XX WPI: 2001-522948/57.

XX N-PSDB; AAH75021.

PS Claim 12; Fig 3; 77pp; English.

CC The present sequence represents fibroblast growth factor 23 (FGF-23).
 CC Human FGF-23 polynucleotides and polypeptides are useful for treating
 CC a patient suffering from traumatic injury or a condition characterized
 CC by dysfunction of or injury to skin cells, a condition characterized by
 CC inadequate function of placental cells (e.g. congenital defects,
 CC fertility, or abnormal growth), a condition characterized by inadequate
 CC function of the thymus (e.g. leukemia, lymphoma, autoimmune disease,
 CC proliferative disorder of the thymus, or differentiation disorder of
 CC the thymus), or a condition characterized by central nervous system
 CC disorder (e.g. Parkinson's disease or Alzheimer's disease). The human
 CC FGF-23 polynucleotide and polypeptide are also useful in the treatment
 CC of Crohn's disease, healing of intestinal wounds, ulcers, inflammation,
 CC injuries and surgical anastomoses, motility and absorption disorders,
 CC and congenital malformations of the intestine. They are also useful for
 CC treating ischemic vascular diseases (e.g. myocardial ischemia/infarction,
 CC peripheral vascular disease, renal artery disease, stroke) and
 CC musculoskeletal disease characterized by loss of function, inadequate
 CC function or death of skeletal muscle cells, bone cells or supporting
 CC cells (e.g. skeletal myopathies, bone disease, or arthritis).

XX Sequence 251 AA;

Query Match 100.0%; Score 1360; DB 22; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7,5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGARLRRLWVCAICSCVCSMSVLRAPVNASPLLGSSWGLHLVTATARNSTYHLQIHKNH 60

DB 1 MLGARLRRLWVCAICSCVCSMSVLRAPVNASPLLGSSWGLHLVTATARNSTYHLQIHKNH 60

QY 61 VDGAHQTIYSALMIRESDAGFVITGVMSRRYLQMDFRGNIGSHYFDPENCFOHQT 120

DB 61 VDGAHQTIYSALMIRESDAGFVITGVMSRRYLQMDFRGNIGSHYFDPENCFOHQT 120

QY 121 ENGQDVVHSPQYHFLVSLGAKRFLPGMPPYSQFLSRNEIPLIHNTPIPRRTR 180

DB 121 ENGQDVVHSPQYHFLVSLGAKRFLPGMPPYSQFLSRNEIPLIHNTPIPRRTR 180

QY 181 AEDSDERDPLNVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVGRVNTAGCTG 240

DB 181 AEDSDERDPLNVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVGRVNTAGCTG 240

QY 241 PEGCRPPAKFI 251

DB 241 PEGCRPPAKFI 251

RESULT 4

AAG63947
 ID AAG63947 standard; Protein; 251 AA.

AC AAG63947;

DT 29-OCT-2001 (first entry)

DE Amino acid sequence of human fibroblast growth factor 23 (FGF-23).

KW Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer;
 KW congenital defect; fertility; thymus; leukemia; lymphoma; injury;
 KW autoimmune disease; proliferative disorder; differentiation disorder;
 KW central nervous system disorder; Parkinson's disease; inflammation;
 KW Alzheimer's disease; Crohn's disease; intestinal wound; stroke;
 KW motility disorder; absorption disorder; intestinal malformation;
 KW ischemic vascular disease; myocardial ischemia; myocardial infarction;
 KW peripheral vascular disease; renal artery disease; skeletal myopathy;
 KW musculoskeletal disease; skeletal muscle cell; bone disease; arthritis.

OS Homo sapiens.

PN WO200166595-A2.

PD 13-SEP-2001.

PF 07-MAR-2001; 2001WO-US07468.

PR 08-MAR-2000; 2000US-0187854.

PR 18-SEP-2000; 2000US-0233368.

PR 05-DEC-2000; 2000US-0251650.

PA (CHIR) CHIRON CORP.

PA (KYOU) UNIV KYOTO.

PI Itoh N, Kavanagh MW;

XX WPI: 2001-522947/57.

XX N-PSDB; AAH75033.

PS Claim 12; Fig 3; 77pp; English.

CC Isolated nucleic acids encoding the human and murine fibroblast growth
 CC factor 23, useful in the treatment of a condition characterized by
 CC inadequate function of placental cells (e.g. congenital defects) and
 CC the thymus (e.g. leukemia) -

CC The present sequence represents fibroblast growth factor 23 (FGF-23).
 CC The human FGF-23 polynucleotide and polypeptide are useful for treating
 CC a patient suffering from traumatic injury or a condition characterized
 CC by dysfunction of or injury to skin cells, a condition characterized
 CC by inadequate function of placental cells (e.g. congenital defects,
 CC fertility, or abnormal growth), a condition characterized by inadequate
 CC function of the thymus (e.g. leukemia, lymphoma, autoimmune disease,
 CC proliferative disorder of the thymus), or differentiation disorder of
 CC the thymus), or a condition characterized by central nervous system
 CC disorder (e.g. Parkinson's disease or Alzheimer's disease). The human
 CC FGF-23 polynucleotide and polypeptide are also useful in the
 CC treatment of Crohn's disease, healing of intestinal wounds, ulcers,
 CC inflammation, injuries and surgical anastomoses, motility and
 CC absorption disorders, and congenital malformations of the intestine.
 CC They are also useful for treating ischemic vascular diseases (e.g.
 CC myocardial ischemia/infarction, peripheral vascular disease, renal
 CC artery disease, stroke) and musculoskeletal disease characterized by
 CC loss of function, inadequate function or death of skeletal muscle cells,
 CC bone cells or supporting cells (e.g. skeletal myopathies, bone disease,
 CC or arthritis).
 CC
 SQ Sequence 251 AA;
 Query Match 100.0%; Score 1360; DB 22; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7.5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGARLRLWCAICSCVSMVLRAYPNASPLIGSSWGLIHLTYTARNSTHLOIHNGH 60
 DB 1 MCGARLRLWCAICSCVSMVLRAYPNASPLIGSSWGLIHLTYTARNSTHLOIHNGH 60
 QY 61 VDGAPHOTISALMIRESDAGFVITGVMSRHYLCMDPRGNI FGSHPEDPENCFOHTL 120
 DB 61 VDGAPHOTISALMIRESDAGFVITGVMSRHYLCMDPRGNI FGSHPEDPENCFOHTL 120
 QY 121 ENGVDVYHSPOYHFLVSLGRKRAFLPGMNPYPYSQPLSRNNEIPLIHFTPIRRHTRS 180
 DB 121 ENGVDVYHSPOYHFLVSLGRKRAFLPGMNPYPYSQPLSRNNEIPLIHFTPIRRHTRS 180
 QY 181 AEDSDSDPLNVLKPRARMPAPASCQELPSADNSPMASDPLGVVGRGVNTHAGGTG 240
 DB 181 AEDSDSDPLNVLKPRARMPAPASCQELPSADNSPMASDPLGVVGRGVNTHAGGTG 240
 QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 5
 AAU12304
 ID AAU12304 standard; Protein; 251 AA.
 XX AAU12304;
 DT 24-OCT-2001. (first entry)
 DE Human PRO9828 polypeptide sequence.
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 OS Homo sapiens.
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GENTH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2001-408281/43.
 DR N-PSDB; AAS21376.
 XX
 PT isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical -
 XX
 PS Claim 12; Fig 266; 813pp; English.
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 CC
 XX
 SQ Sequence 251 AA;
 Query Match 100.0%; Score 1360; DB 22; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7.5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGARLRLWCAICSCVSMVLRAYPNASPLIGSSWGLIHLTYTARNSTHLOIHNGH 60
 DB 1 MCGARLRLWCAICSCVSMVLRAYPNASPLIGSSWGLIHLTYTARNSTHLOIHNGH 60

QY 61 VDGAPHOTIYSALMIRESDAGFVVITGWSRRYLCDPFRGNIFGSHYDPENCRFQHOTL 120
 DB 61 VDGAPHOTIYSALMIRESDAGFVVITGWSRRYLCDPFRGNIFGSHYDPENCRFQHOTL 120
 QY 121 ENGVDVYHSPQYHFLVSLGRAKRAFLPGMNPYPYSGFLSRNNEIPLIHFTPIPRRHTRS 180
 DB 121 ENGVDVYHSPQYHFLVSLGRAKRAFLPGMNPYPYSGFLSRNNEIPLIHFTPIPRRHTRS 180
 QY 181 AEDDSEKDPPLNVLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVVGRGVNTHAGGTG 240
 DB 181 AEDDSEKDPPLNVLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVVGRGVNTHAGGTG 240
 QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 6
 AAB84652
 ID AAB84652 standard; Protein; 251 AA.
 AC AAB84652;
 DT 05-SEP-2001 (first entry)
 DE Amino acid sequence of fibroblast growth factor homologue zFGF12.
 KW Fibroblast growth factor; FGF; zFGF12; chromosome 12; 12q.1.3;
 KW neuronal cell; prostatic cell; pancreatic cell; haematopoietic cell;
 KW hyperplasia; regeneration; diabetes; amyotrophic lateral sclerosis;
 KW stroke; angiogenesis; wound healing.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /note= "signal peptide"
 FT Protein /note= "mature protein"
 PN WO200149740-A1.
 PD 12-JUL-2001.
 PF 04-JAN-2001; 2001WO-US00238.
 PR 05-JAN-2000; 2000US-0478062.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Conklin DC;
 XX WPI; 2001-418357/44.
 DR N-PSDB; AAH28133.
 PT A fibroblast growth factor homolog polypeptide zFGF12 and the nucleic
 PT acids that encode it, useful for preventing, diagnosing and controlling
 PT e.g. diabetes, amyotrophic lateral sclerosis, strokes, angiogenesis
 PT and wound healing -
 PS Claim 4; Page 60-61; 66pp; English.
 CC The present sequence represents a human fibroblast growth factor (FGF)
 CC homologue, designated zFGF12. The zFGF12 polypeptides contain a motif
 CC (see AAB84654) that occurs in all known members of the FGF family, which
 CC is unique to these proteins. This motif is highly conserved in all
 CC members of the FGF family, however, zFGF12 appears to be unique in that
 CC the conserved Glu is a His (residue 117) substituting a basic amino
 CC acid (aa) residue for an acidic aa residue. The zFGF12 gene is mapped
 CC to chromosome 12, location 12q.1.3. zFGF12 may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate FGF expression. Disorders and processes that may be
 CC prevented, diagnosed, and treated include, for example proliferation

CC of neuronal, prostatic and pancreatic tissue cells, growth and
 CC differentiation of haematopoietic cells, hyperplasia and regeneration,
 CC diabetes, amyotrophic lateral sclerosis, strokes, angiogenesis and
 CC wound healing.
 CC XX
 SQ Sequence 251 AA;
 Query Match 100.0%; Score 1360; DB 22; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7, 5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAGRLMLWCALCSVCSMSVLRAPNASPLGSSWGLHLHTATARNYHLQIHNGH 60
 DB 1 MLAGRLMLWCALCSVCSMSVLRAPNASPLGSSWGLHLHTATARNYHLQIHNGH 60
 QY 61 VDGAPHOTIYSALMIRESDAGFVVITGWSRRYLCDPFRGNIFGSHYDPENCRFQHOTL 120
 DB 61 VDGAPHOTIYSALMIRESDAGFVVITGWSRRYLCDPFRGNIFGSHYDPENCRFQHOTL 120
 QY 121 ENGVDVYHSPQYHFLVSLGRAKRAFLPGMNPYPYSGFLSRNNEIPLIHFTPIPRRHTRS 180
 DB 121 ENGVDVYHSPQYHFLVSLGRAKRAFLPGMNPYPYSGFLSRNNEIPLIHFTPIPRRHTRS 180
 QY 181 AEDDSEKDPPLNVLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVVGRGVNTHAGGTG 240
 DB 181 AEDDSEKDPPLNVLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVVGRGVNTHAGGTG 240
 QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 7
 AAG89178
 ID AAG89178 standard; Protein; 251 AA.
 AC AAG89178;
 DT 11-SEP-2001 (first entry)
 DE Human secreted protein, SEQ ID NO: 298.
 KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
 KW GENSET.
 OS Homo sapiens.
 PN WO200142451-A2.
 PD 14-JUN-2001.
 PF 07-DEC-2000; 2000WO-IB01938.
 PR 08-DEC-1999; 99US-0163629.
 PR 06-MAR-2000; 2000US-0187470.
 PA (GENSET) GENSET.
 PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
 XX WPI; 2001-367870/38.
 DR N-PSDB; AAH64781.
 PT Full length GENSET human nucleic acids encoding potentially secreted
 PT proteins, useful in gene therapy and vaccination against a variety of
 PT diseases, and for diagnosis of those diseases -
 PS Claim 21; Page 828-829; 921pp; English.
 CC The invention relates to full length GENSET human nucleic acids encoding
 CC potentially secreted proteins. The nucleic acids and the polypeptides
 CC they encode may be used in the prevention, treatment and diagnosis of
 CC diseases associated with inappropriate GENSET gene expression. For

CC example, they be used to treat disorders associated with decreased
 CC GENSER gene expression by rectifying mutations or deletions in a
 CC patient's genome that affect the activity of GENSER or by supplementing
 CC the patient's own production of GENSER polypeptides. Conversely,
 CC antisense nucleic acid molecules may be administered to down regulate
 CC GENSER expression by binding with the cells' own genes and preventing
 CC their expression. The sense and antisense nucleic acids may also be
 CC used as DNA probes in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples, and hence to
 CC determine which patients may be in need of restorative therapy.
 CC The GENSER polypeptides may be used as antigens in the production of
 CC antibodies and in assays to identify modulators (agonists and
 CC antagonists) of GENSER polypeptide expression and activity. The
 CC present sequence is a GENSER polypeptide of the invention.

Sequence 251 AA;

Query Match 100.0%; Score 1360; DB 22; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7.5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGARLRLWVLCALCSVCSMSVLAAYPNASPLLGSSWGGLHLTYATARNSYHLQIHKNHG 60
 DB 1 MCGARLRLWVLCALCSVCSMSVLAAYPNASPLLGSSWGGLHLTYATARNSYHLQIHKNHG 60
 QY 61 VDGAPHQTIYSALMIRSEDAFVVITGVMSRRYLCDMFRNIGSHYFDPENCRFQHOTL 120
 DB 61 VDGAPHQTIYSALMIRSEDAFVVITGVMSRRYLCDMFRNIGSHYFDPENCRFQHOTL 120
 QY 121 ENGVDVYHSPQYHFLVSLGAKAKAFPLPGMNPYPYQFLSRNNEIPLIHFTPIPRRHTRS 180
 DB 121 ENGVDVYHSPQYHFLVSLGAKAKAFPLPGMNPYPYQFLSRNNEIPLIHFTPIPRRHTRS 180
 QY 181 AEDDSERDPLNLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVYRGGRVNTHAGGTG 240
 DB 181 AEDDSERDPLNLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVYRGGRVNTHAGGTG 240
 QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 8
 ID AAB65297 standard; Protein; 251 AA.
 XX AAB65297;
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO9828 protein sequence SEQ ID NO:511.
 XX
 KM Human; secreted and transmembrane protein; PRO; cytosolic;
 KM cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KM diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000MO-US08439.
 XX
 PR 02-JUN-1999; 99MO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99MO-US21090.
 PR 15-SEP-1999; 99MO-US21547.

PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28301.
 PR 16-DEC-1999; 99MO-US30095.
 PR 20-DEC-1999; 99MO-US30919.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US04914.
 PR 24-FEB-2000; 2000MO-US05004.
 PR 02-MAR-2000; 2000MO-US05841.
 PR 15-MAR-2000; 2000MO-US06884.
 PR 20-MAR-2000; 2000MO-US07377.

XX (GENETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Kijavini TJ, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tamas D, Watande CK, Williams PM, Wood WI,
 PI Zhang Z;

DR WPI; 2001-032160/04.
 DR N-PDSB; AAF44266.

PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -

PS Claim 12; Fig 324; 935pp; English.

XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomes and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.

Sequence 251 AA;

Query Match 100.0%; Score 1360; DB 22; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7.5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGARLRLWVLCALCSVCSMSVLAAYPNASPLLGSSWGGLHLTYATARNSYHLQIHKNHG 60
 DB 1 MCGARLRLWVLCALCSVCSMSVLAAYPNASPLLGSSWGGLHLTYATARNSYHLQIHKNHG 60
 QY 61 VDGAPHQTIYSALMIRSEDAFVVITGVMSRRYLCDMFRNIGSHYFDPENCRFQHOTL 120
 DB 61 VDGAPHQTIYSALMIRSEDAFVVITGVMSRRYLCDMFRNIGSHYFDPENCRFQHOTL 120
 QY 121 ENGVDVYHSPQYHFLVSLGAKAKAFPLPGMNPYPYQFLSRNNEIPLIHFTPIPRRHTRS 180
 DB 121 ENGVDVYHSPQYHFLVSLGAKAKAFPLPGMNPYPYQFLSRNNEIPLIHFTPIPRRHTRS 180
 QY 181 AEDDSERDPLNLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVYRGGRVNTHAGGTG 240
 DB 181 AEDDSERDPLNLKPRARMTAPAPASCQELPSAEDNSPMASDPLGVYRGGRVNTHAGGTG 240
 QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 9

ID ABB77581 standard; Protein; 251 AA.

AC ABB77581;

DT 26-AUG-2002 (first entry)

DE Human FGF23 protein SEQ ID NO 2.

KW Human; FGF23; haemostatic; hyperphosphataemia; gene therapy.

OS Homo sapiens.

PN WO00252009-A1.

PD 04-JUL-2002.

PF 26-DEC-2001; 2001WO-JP11482.

PR 26-DEC-2000; 2000JP-0396316.

PR 29-MAY-2001; 2001JP-0161370.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Itoh H, Fukushima N, Saito H, Kusano K;

DR WPI; 2002-50891/54.

DR N-PSDB; ABBN1575.

PT Human FGF23 protein mutant for lowering blood phosphorus level,
PT applicable in gene therapy remedies for hyperphosphatemia -

PS Claim 1, Page 46-48; 64pp; Japanese.

CC The invention relates to a DNA (ABN81575) encoding a protein (ABB77581)
CC FGF23 and mutants FGF23 comprising an amino acid substitution of arginine
CC at position 176 to glutamine and/or position 179 to glutamine or
CC tryptophan. The mutants are generated by introducing the following base
CC changes in the nucleic acid sequence: R176Q mutant is generated by
CC G527A; R179Q is generated by G536A; and R179W is generated by C535T. The
CC protein and encoding DNA are applicable in remedies for
CC hyperphosphatemia, including gene therapy.

SQ Sequence 251 AA;

Query Match 100.0%; Score 1360; DB 23; Length 251;

Best Local Similarity 100.0%; Pred. No. 7, 5e-131;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARLRWVWALCSVCSMSVLAAYPNASPLSSWGGLHLYTATRNSTYHQLIHNKH 60
DB 1 MGARLRWVWALCSVCSMSVLAAYPNASPLSSWGGLHLYTATRNSTYHQLIHNKH 60
QY 61 VDCAPHQITYSALMIRSEDAQFVIVGWSRRYLQWDFRNGSHVFEDENCRFHQTL 120
DB 61 VDCAPHQITYSALMIRSEDAQFVIVGWSRRYLQWDFRNGSHVFEDENCRFHQTL 120
QY 121 ENGVDYVHSPOVHFLVSLGAKRAFLPGMNPYPYSQFLSRNRIPLIHFTPIPRRTRS 180
DB 121 ENGVDYVHSPOVHFLVSLGAKRAFLPGMNPYPYSQFLSRNRIPLIHFTPIPRRTRS 180
QY 181 AEDDSRDPPLNVLKPRARMTPADSCSQELPSAEDNSPMASDPLGVVGRGVNTHAGTGS 240
DB 181 AEDDSRDPPLNVLKPRARMTPADSCSQELPSAEDNSPMASDPLGVVGRGVNTHAGTGS 240
QY 241 PEGCRPEFAKFI 251
DB 241 PEGCRPEFAKFI 251

RESULT 10

ID AAU79355 standard; Protein; 251 AA.

AC AAU79355;

DT 02-JUL-2002 (first entry)

DE Human fibroblast growth factor-23 (FGF23).

KW Fibroblast growth factor 23; FGF23; hypophosphataemic disorder;

KW autosomal dominant hypophosphataemic rickets; ADHR; fibrous dysplasia;

KW X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia;

KW TIO; hereditary hypophosphataemic rickets with hypocalciuria; HHRH;

KW hypophosphataemic bone disease; HBD; epidermal nevus syndrome;

KW nephrolithiasis; hyperphosphataemic disorder; mild renal insufficiency;

KW tumoural calcinosis; osteoporosis; dermatomyositis; human.

OS Homo sapiens.

PN WO00208271-A1.

PD 31-JAN-2002.

PF 10-JUL-2001; 2001WO-US21738.

PR 19-JUL-2000; 2000US-219137P.

PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

PI (UYMG-) UNIV MOENCHEN MAXIMILIANS LUDWIG.

DR Ebone M, White K, Strom TM, Meltinger T;

DR WPI; 2002-329399/36.

DR N-PSDB; ABK48318.

PT Novel fibroblast growth factor 23, and polynucleotides encoding the

PT polypeptides, useful for treating hyperphosphataemic disorders such as

PT mild renal insufficiency or tumoural calcinosis, or coronary artery

PS disease -

PS Claim 3; Fig 9; 130pp; English.

CC The invention describes an isolated polypeptide (I) comprising a
CC fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant,
CC homologue or fragment. (I) is useful for treatment of a hypophosphataemic
CC disorder such as autosomal dominant hypophosphataemic rickets (ADHR),
CC X-linked hypophosphataemic rickets (XLH), hereditary hypophosphataemic
CC rickets with hypocalciuria (HHRH), hypophosphataemic bone disease (HBD),
CC epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia
CC (TIO), and nephrolithiasis. (I) can also be used in treatment of a
CC hypophosphataemic disorder such as mild renal insufficiency and tumoural
CC calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving
CC deposition of calcium and phosphate in the arteries or soft tissues of
CC mammal, coronary artery disease may also be treated using methods
CC described in the invention. Preferably, the nucleic acid or the
CC polypeptide comprises a mutation that confers increased stability on
CC FGF23 polypeptide. The polynucleotide encoding (I) can be used in gene
CC therapy to treat diseased individuals. This is the amino acid sequence
CC of the novel human fibroblast growth factor 23 (FGF23) studied in the
CC invention.

SQ Sequence 251 AA;

Query Match 100.0%; Score 1360; DB 23; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7.5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARLRLWVCAICVCSMSVLRAYPNASPLIGSSWGGLHLVTATARNSTYHLQIHKNKH 60
 DB 1 MGARLRLWVCAICVCSMSVLRAYPNASPLIGSSWGGLHLVTATARNSTYHLQIHKNKH 60
 QY 61 VDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLQMDPRGNIFGSHYDPDENCRFQHOTL 120
 DB 61 VDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLQMDPRGNIFGSHYDPDENCRFQHOTL 120
 QY 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPYPYSQFLSRNEIPLIHFTPIPRRHTRS 180
 DB 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPYPYSQFLSRNEIPLIHFTPIPRRHTRS 180
 QY 181 AEDSERDPLNVLKPRRMTFAPASCQELPSAEDNSPMASDPLGVVGRVNTAGGTG 240
 DB 181 AEDSERDPLNVLKPRRMTFAPASCQELPSAEDNSPMASDPLGVVGRVNTAGGTG 240
 QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 11
 ABB06940
 ID ABB06940 standard; Protein; 251 AA.
 AC ABB06940;
 DT 19-JUN-2002 (first entry)
 DE Human OSTF31 protein sequence SEQ ID NO:2.
 XX
 XX OSTF31; phosphoric acid metabolism; calcium metabolism; calcification;
 KM vitamin D metabolism; hypophosphataemia; phosphate transport; cytosolic;
 KM chromosome 12p13; osteoparatic; nephrotropic; antihyperphosphataemic;
 KM phosphorus transport; skeletal disorder; bone cancer; osteoporosis;
 KM bone formation abnormality; vitamin D resistance; Paget's disease;
 KM bone calcium deficiency; kidney disorder; kidney function deficiency;
 KM renal phosphate leakage; urinary tubule acidosis; Fanconi's disease.
 OS Homo sapiens.
 XX
 XX
 PN WO200214504-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-JP06944.
 XX
 PR 11-ANG-2000; 2000JP-0245144.
 PR 21-SEP-2000; 2000JP-0287684.
 PR 22-DEC-2000; 2000JP-0391077.
 PR 19-APR-2001; 2001JP-0121527.
 XX
 XX (KIRI) KIRIN BEER KK.
 PA
 PA Yamashita T, Shimada T, Mizutani S, Fukumoto S;
 PI
 PI WPI; 2002-227350/28.
 DR N-PSDB; ABL50577.
 DR
 XX
 XX Polypeptides useful for regulating phosphate transport and calcium
 PT metabolism and DNA encoding them for treatment of phosphate and calcium
 PT metabolism disorders, including bone formation abnormalities and kidney
 PT diseases
 XX
 PS Claim 1; Page 158-159; 221pp; Japanese.
 CC The present invention describes DNA encoding a polypeptide having the
 CC activities of inhibiting hypophosphataemia, phosphate transport and
 CC calcification, and regulating vitamin D metabolism in vivo. The

CC polypeptide is of human origin (designated OSTF31) which is localised to
 CC chromosome 12p13, or is derived from this by addition, deletion and/or
 CC substitution of one or more amino acid residues. OSTF31 has osteoparatic,
 CC nephrotropic, antihyperphosphataemic and cytosolic activities. The
 CC OSTF31 polypeptide regulates phosphorus transport and calcium metabolism.
 CC OSTF31 sequences can be used for the treatment and diagnosis of skeletal
 CC disorders such as bone cancer, bone formation abnormalities, vitamin D
 CC resistance, osteoporosis, Paget's disease and bone calcium deficiency;
 CC kidney disorders such as kidney function deficiency, renal phosphate
 CC leakage, urinary tubule acidosis and Fanconi's disease. The present
 CC sequence is used in the exemplification of the present invention.

QY Sequence 251 AA;
 SQ

Query Match 100.0%; Score 1360; DB 23; Length 251;
 Best Local Similarity 100.0%; Pred. No. 7.5e-131;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARLRLWVCAICVCSMSVLRAYPNASPLIGSSWGGLHLVTATARNSTYHLQIHKNKH 60
 DB 1 MGARLRLWVCAICVCSMSVLRAYPNASPLIGSSWGGLHLVTATARNSTYHLQIHKNKH 60
 QY 61 VDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLQMDPRGNIFGSHYDPDENCRFQHOTL 120
 DB 61 VDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLQMDPRGNIFGSHYDPDENCRFQHOTL 120
 QY 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPYPYSQFLSRNEIPLIHFTPIPRRHTRS 180
 DB 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPYPYSQFLSRNEIPLIHFTPIPRRHTRS 180
 QY 181 AEDSERDPLNVLKPRRMTFAPASCQELPSAEDNSPMASDPLGVVGRVNTAGGTG 240
 DB 181 AEDSERDPLNVLKPRRMTFAPASCQELPSAEDNSPMASDPLGVVGRVNTAGGTG 240
 QY 241 PEGCRPPAKFI 251
 DB 241 PEGCRPPAKFI 251

RESULT 12
 ABB08352
 ID ABB08352 standard; Protein; 251 AA.
 AC ABB08352;
 DT 18-JUN-2002 (first entry)
 DE Human zFGF12 amino acid sequence.
 XX
 XX
 XX
 XX zFGF12; human; fibroblast growth factor; FGF; vulnerrary; chemotherapy;
 KM lung injury; epithelial cell; mesenchymal cell.
 KM
 OS Homo sapiens.
 XX
 XX
 FH Key
 FH Peptide
 FT 1..24 Location/Qualifiers
 FT /label= secretory_signal_sequence
 FT 2..51
 FT /label= beta-strand_1
 FT 3..59
 FT /label= beta-strand_2
 FT 4..71
 FT /label= beta-strand_3
 FT 5..81
 FT /label= beta-strand_4
 FT 6..92
 FT /label= beta-strand_5
 FT 7..99
 FT /label= beta-strand_6
 FT 8..113
 FT /label= beta-strand_7
 FT 9..123
 FT /label= beta-strand_8

PS Example 2; Page -; 64pp; Japanese.

XX The invention relates to a DNA (ABN81575) encoding a protein (ABB77581).

CC FGFP23 and mutants FGFP23 comprising an amino acid substitution of arginine

CC at position 176 to glutamine and/or position 179 to glutamine or

CC tryptophan. The mutants are generated by introducing the following base

CC changes in the nucleic acid sequence: R176Q mutant is generated by

CC G527A; R179Q is generated by G536A; and R179W is generated by C535T. The

CC protein and encoding DNA are applicable in remedies for

CC hyperphosphataemia, including gene therapy. The present sequence is that

CC of a FGFP23 mutant of the invention.

CC Note: The present sequence is not shown in the specification but is

CC derived from the wildtype human FGFP23 sequence given as SEQ ID NO 2 in

CC the sequence listing (ABB77581).

XX Sequence 251 AA;

SQ

Query Match 99.7%; Score 1356; DB 23; Length 251;

Best Local Similarity 99.6%; Pred. No. 1.9e-130;

Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGARLRLWVCAICSCVCSMSVLAAYPNASPLLGSSWGLIHLVTATARNSYHLQIHKNHG 60

DB 1 MCGARLRLWVCAICSCVCSMSVLAAYPNASPLLGSSWGLIHLVTATARNSYHLQIHKNHG 60

QY 61 VDAAPHOTIYSALMIRSEDAFGVITGVMSRRYLCPDFRNIGSHYFDPENCRFOHOTL 120

DB 61 VDAAPHOTIYSALMIRSEDAFGVITGVMSRRYLCPDFRNIGSHYFDPENCRFOHOTL 120

QY 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPFPYSOPLSRNEIPLIHFTPIPRRHTRS 180

DB 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPFPYSOPLSRNEIPLIHFTPIPRRHTRS 180

QY 181 AEDDSERDPLNVLKPRARMTAPAPASCSOELPSAEDNSPMASDPLGVVGRVNTHAGTG 240

DB 181 AEDDSERDPLNVLKPRARMTAPAPASCSOELPSAEDNSPMASDPLGVVGRVNTHAGTG 240

QY 241 PEGCRPPAKFI 251

DB 241 PEGCRPPAKFI 251

RESULT 14

ABB77583

ID ABB77583 standard; Protein; 251 AA.

XX ABB77583;

AC 28-AUG-2002 (first entry)

XX

DE Human FGFP23 mutant R179Q.

XX

KW Human; FGFP23; haemostatic; hyperphosphataemia; gene therapy; mutant;

KW mutain.

XX

OS Homo sapiens.

OS Synthetic.

XX

FT Key Location/Qualifiers

FT Misc-difference 179 /note="Wildtype Arg substituted by Gln"

XX

PN WO200252009-A1.

XX

PD 04-JUL-2002.

XX

PF 26-DEC-2001; 2001WO-JP11482.

XX

PR 26-DEC-2000; 2000JP-0396316.

XX

PR 29-MAY-2001; 2001JP-0161370.

XX

PA (CHUS) CHUGAI SEIRYAKU KK.

XX

PI Itoh H, Fukushima N, Saito H, Kusano K;

XX WPI; 2002-508891/54.

DR

XX Human FGFP23 protein mutant for lowering blood phosphorus level,

PT applicable in gene therapy remedies for hyperphosphataemia -

XX

PS Example 2; Page -; 64pp; Japanese.

XX

CC The invention relates to a DNA (ABN81575) encoding a protein (ABB77581)

CC FGFP23 and mutants FGFP23 comprising an amino acid substitution of arginine

CC at position 176 to glutamine and/or position 179 to glutamine or

CC tryptophan. The mutants are generated by introducing the following base

CC changes in the nucleic acid sequence: R176Q mutant is generated by

CC G527A; R179Q is generated by G536A; and R179W is generated by C535T. The

CC protein and encoding DNA are applicable in remedies for

CC hyperphosphataemia, including gene therapy. The present sequence is that

CC of a FGFP23 mutant of the invention.

CC Note: The present sequence is not shown in the specification but is

CC derived from the wildtype human FGFP23 sequence given as SEQ ID NO 2 in

CC the sequence listing (ABB77581).

XX Sequence 251 AA;

SQ

Query Match 99.7%; Score 1356; DB 23; Length 251;

Best Local Similarity 99.6%; Pred. No. 1.9e-130;

Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGARLRLWVCAICSCVCSMSVLAAYPNASPLLGSSWGLIHLVTATARNSYHLQIHKNHG 60

DB 1 MCGARLRLWVCAICSCVCSMSVLAAYPNASPLLGSSWGLIHLVTATARNSYHLQIHKNHG 60

QY 61 VDAAPHOTIYSALMIRSEDAFGVITGVMSRRYLCPDFRNIGSHYFDPENCRFOHOTL 120

DB 61 VDAAPHOTIYSALMIRSEDAFGVITGVMSRRYLCPDFRNIGSHYFDPENCRFOHOTL 120

QY 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPFPYSOPLSRNEIPLIHFTPIPRRHTRS 180

DB 121 ENGVDVHSPQYHFLVSLGAKRAFLPGMNPFPYSOPLSRNEIPLIHFTPIPRRHTRS 180

QY 181 AEDDSERDPLNVLKPRARMTAPAPASCSOELPSAEDNSPMASDPLGVVGRVNTHAGTG 240

DB 181 AEDDSERDPLNVLKPRARMTAPAPASCSOELPSAEDNSPMASDPLGVVGRVNTHAGTG 240

QY 241 PEGCRPPAKFI 251

DB 241 PEGCRPPAKFI 251

RESULT 15

AAU79379

ID AAU79379 standard; Protein; 251 AA.

XX AAU79379;

AC 02-JUL-2002 (first entry)

XX

DE Human fibroblast growth factor-23 (FGFP23), R176Q mutant.

XX

KW Fibroblast growth factor 23; FGFP23; hypophosphataemic disorder;

KW autosomal dominant hypophosphataemic rickets; ADHR; fibrous dysplasia;

KW X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia;

KW TIO; hereditary hypophosphataemic rickets with hypercalciuria; HHRH;

KW hypophosphataemic bone disease; HBD; epidermal nevus syndrome;

KW nephrocalcinosis; hyperphosphataemic disorder; mild renal insufficiency;

KW tumoral calcinosis; osteoporosis; dermatomyositis; human; mutant;

KW mutain.

XX

OS Homo sapiens.

OS Synthetic.

XX

FT Key Location/Qualifiers

FT Misc-difference 176

Search completed: May 23, 2003, 07:43:14
Job time : 77 sec

FT /note= "Wild type Arg substituted by Gln"
XX
PN W0200208271-A1.
XX
PD 31-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-US21738.
XX
PR 19-JUL-2000; 2000US-219137P.
XX
PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX (UYMU-) UNIV MUEBCHEN MAXIMILIANS LUDWIG.
XX
PI Econs M, White K, Strom TM, Meltinger T;
XX WPI; 2002-329399/36.
XX
DR Novel fibroblast growth factor 23, and polynucleotides encoding the
XX PT polypeptides, useful for treating hyperphosphataemic disorders such as
XX PT mild renal insufficiency or tumoural calcinosis, or coronary artery
XX PT disease -
XX
XX Example 1; Page -; 130pp; English.
XX
CC The invention describes an isolated polypeptide (I) comprising a
CC fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant,
CC homologue or fragment. (I) is useful for treatment of a hypophosphataemic
CC disorder such as autosomal dominant hypophosphataemic rickets (ADHR),
CC X-linked hypophosphataemic rickets (XLRH), hereditary hypophosphataemic
CC rickets with hypercalciuria (HHRH), hypophosphataemic bone disease (HBD),
CC epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia
CC (FIO), and nephrolithiasis. (I) can also be used in treatment of a
CC hyperphosphataemic disorder such as mild renal insufficiency and tumoural
CC calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving
CC deposition of calcium and phosphate in the arteries or soft tissues of
CC mammal, coronary artery disease may also be treated using methods
CC described in the invention. Preferably, the nucleic acid or the
CC polypeptide comprises a mutation that confers increased stability on
CC FGF23 polypeptide. The polynucleotide encoding (I) can be used in gene
CC therapy to treat diseased individuals. This sequence represents a mutant
CC of the novel human fibroblast growth factor 23 (FGF23) used to study
CC residues in the predicted protease cleavage site.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79355 using information
CC given in example 1 of the invention.
XX
XX
SQ Sequence 251 AA;

Query Match 99.7%; Score 1356; DB 23; Length 251;
Best Local Similarity 99.6%; Pred. No. 1.9e-130;
Matches 250; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGARLRIMVCAICGVCMSVLRAPNAPSLIGSSWGLIHLTYTARNSTHLQIHKNH 60
DB 1 MLGARLRIMVCAICGVCMSVLRAPNAPSLIGSSWGLIHLTYTARNSTHLQIHKNH 60
QY 61 VDGAPHOTIYALMIRSEDAGFVITGVMSRRYLICMDFRGNIFGSHYDPENCROHOTL 120
DB 61 VDGAPHOTIYALMIRSEDAGFVITGVMSRRYLICMDFRGNIFGSHYDPENCROHOTL 120
QY 121 ENGDDVYHSPQYHFLVSLGKRAKRAFLPGMNPYPYSQFLSRNEIPLIHNTPIPRRHTRS 180
DB 121 ENGDDVYHSPQYHFLVSLGKRAKRAFLPGMNPYPYSQFLSRNEIPLIHNTPIPRRHTRS 180
QY 181 AEDDSEDPPLAVLAKPRAMTPAPASCSOELPSAEDNSPMAADPLGAVRGRVNTAGGTG 240
DB 181 AEDDSEDPPLAVLAKPRAMTPAPASCSOELPSAEDNSPMAADPLGAVRGRVNTAGGTG 240
QY 241 PEGCRPPAKFI 251
DB 241 PEGCRPPAKFI 251